SEQUENCE LISTING

<110>	Elich Volra Weath	th,	Sand	ra L		C.									
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gag gt Glu Va	a ccc al Pro	ggt Gly 100	ggc Gly	tct Ser	aac Asn	aac Asn	aac Asn 105	aac Asn	tac Tyr	gct Ala	aac Asn	gtc Val 110	gac Asp	ctc Leu	336
atc gt Ile Va	cc gat al Asp 115	Val	gct Ala	gag Glu	cga Arg	gcc Ala 120	Gly	gtt Val	cac His	gcc Ala	gta Val 125	tgg Trp	gct Ala	ggc Gly	384

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cga Arg	aag Lys	tgt Cys	acc Thr	aac Asn 245	ggc Gly	gaa Glu	gaa Glu	ttc Phe	aag Lys 250	cag Gln	ctc Leu	tac Tyr	aac Asn	gcc Ala 255	gtt Val	768
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				Thr					Tyr		ccc Pro			Gly	gag Glu	1056
			Leu					Arg			gtc Val		His		act Thr	1104

					ggt Gly											1152
_	_				ctc Leu 390								_			1200
					ggt Gly											1248
		_			acc Thr										gta Val	1296
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Gly	Met	Gly	Ala	Leu	act Thr	Glu	Leu	Asn	Phe	Arg	Ser	Ser				1392
	Gly				gtc Val 470											1440
_	_	_			cac His					_						1488
	_		_		gtc Val											1536
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- Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 50 55 60
- Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu 65 70 75 80
- Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val 85 90 95
- Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110
- Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
 115 120 125
- Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala 130 135 140
- Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg 145 150 155 160
- Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp 165 170 175
- Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met 180 185 190
- Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala 195 200 205
- Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly 210 220
- Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile 225 230 235 240
- Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val 245 250 255
- Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly 260 265 270

Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val 425 430 Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly

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Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp

140

135

130

					act Thr 150					_						480
					gca Ala											528
_	_		_		gtg Val								_		_	576
					gaa Glu											624
					gac Asp								_		_	672
					atg Met 230										aag Lys 240	720
					cac His										_	768
				_	atc Ile							_	-	_	_	816
					cac His											864
					ctc Leu				_	_		_	_	_	_	912
		_		_	gag Glu 310	_			_						-	960
_			_	_	atg Met	_	_	_		_		_	_		_	1008
_		_			ggt Gly		_			_		_		_	_	1056
					tcg Ser					_			_	_	_	1104
					gtc Val			_								1152
gct	gct	caa	ctg	caa	gtg	gct	atg	ggt	att	ccg	ctg	cac	tgc	atc	ccg	1200

Ala Ala Gln I 385	Leu Gln Val 390		Gly Ile	Pro Leu 395	His Cys	Ile Pro 400	
gat gtg cgt o Asp Val Arg A							1248
gac ttc gac g Asp Phe Asp A	gcg gag aag Ala Glu Lys 420	cag aag Gln Lys	cca ccg Pro Pro 425	cat gga His Gly	cac gtt His Val 430	atc gcc Ile Ala	1296
gcg cgt att a Ala Arg Ile 1 435			Asn Ala				1344
gga gcc atc o Gly Ala Ile o 450							1392
tac ttc tcg of Tyr Phe Ser 1		Ser Gly					1440
cag att ggt (Gln Ile Gly)							1488
aag aac atg g Lys Asn Met							1536
cac acg acg His Thr Thr 515			Asn Met				1584
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Tyr Val Arg 35	Leu Gln Ly	s Gly Thr 40	Arg Pro	Ile Thr	Ser Val 45	Leu Ile	

Ala Asn Ası 50	n Gly Ile	Ser Ala 55	Val	Lys	Ala	Ile	Arg 60	Ser	Ile	Arg	Ser
Trp Ser Ty:	r Glu Met	Phe Ala 70	Asp	Glu	His	Val 75	Val	Thr	Phe	Val	Val 80
Met Ala Th	r Pro Glu 85	Asp Leu	Lys	Ala	Asn 90	Ala	Glu	Tyr	Ile	Arg 95	Met
Ala Glu Hi	s Val Val 100	Glu Val	Pro	Gly 105	Gly	Ser	Asn	Asn	His 110	Asn	Tyr
Ala Asn Vai		Ile Ile	Glu 120	Ile	Ala	Glu	Arg	Phe 125	Asn	Val	Asp
Ala Val Tr	o Ala Gly	Trp Gly		Ala	Ser	Glu	Asn 140	Pro	Leu	Leu	Pro
Asp Thr Le	ı Ala Gln	Thr Glu	Arg	Lys	Ile	Val 155	Phe	Ile	Gly	Pro	Pro 160
Gly Lys Pro	o Met Arg 165		Gly	Asp	Lys 170	Ile	Gly	Ser	Thr	Ile 175	Ile
Ala Gln Se	r Ala Lys 180	Val Pro	Thr	Ile 185	Ala	Trp	Asn	Gly	Asp 190	Gly	Met
Glu Val Asy		Glu His	Asp 200	Gly	Ile	Pro	Asp	Glu 205	Ile	Tyr	Asn
Ala Ala Me	t Leu Arg	Asp Gly 215		His	Cys	Leu	Asp 220	Glu	Суз	Lys	Arg
Ile Gly Pho 225	e Pro Val	Met Ile 230	Lys	Ala	Ser	Glu 235	Gly	Gly	Gly	Gly	Lys 240
Gly Ile Ar	g Met Val 245		Glu	Ser	Gln 250	Val	Leu	Ser	Ala	Trp 255	Glu
Ala Val Ar	g Gly Glu 260	Ile Pro	Gly	Ser 265	Pro	Ile	Phe	Val	Met 270	Lys	Leu
Ala Pro Ly	_	His Leu	Glu 280	Val	Gln	Leu	Leu	Ala 285	Asp	Thr	Tyr

Gly Asn Ala Ile Ala Leu Ser Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Val Glu Glu Gly Pro Val Leu Ala Pro Thr Gln Glu Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe

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His Asn Glu Val Arg Leu Gln Gly Arg Pro Asp 545 550 555

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						tct Ser										624
						tcg Ser 215										672
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						gag Glu										864
						tcg Ser 295										912
						gtg Val										960
						cgt Arg	-	_								1008
aaq									330							
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Lys aag Lys gtc	gcc Ala	atg Met 355	Glu 340 gag Glu ggt	Glu gag Glu acc	Ala gcc Ala gtc	Pro gct	yal gtt Val 360	Thr 345 cgt Arg	atc Ile ctt Leu	Ala ggt Gly tcg	cgt Arg	ctt Leu 365	Asp 350 gtc Val gac	acg Thr ggt Gly	tac Tyr	
Lys aag Lys gtc Val	gcc Ala tct Ser 370 tac	atg Met 355 gct Ala	Glu 340 gag Glu ggt Gly	gag Glu acc Thr	gcc Ala gtc Val	gct Ala gag Glu	yal gtt val 360 tac Tyr	Thr 345 cgt Arg ctg Leu	atc Ile ctt Leu tac Tyr	ggt Gly tcg ser	cgt Arg cac His 380	ctt Leu 365 gcc Ala	Asp 350 gtc Val gac Asp	acg Thr ggt Gly gac Asp	tac Tyr aag Lys	1104

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			ca tcg ccc aaa g Pro Ser Pro Lys (460	-
			ect gga gag ggc t Pro Gly Glu Gly I 475	
		Leu Asn P	tc cgc agt agt the Arg Ser Ser S	_ -
Trp Gly Tyr F			gt gga att cac a Sly Gly Ile His S	
			at ggc gag aac d yr Gly Glu Asn A	
		_	ag gaa ctt agc a ys Glu Leu Ser I 540	
			tc aag ctt ctg c le Lys Leu Leu 6 555	
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Leu	Glu 50	Asn	Ala	Pro	Pro	Ser 55	Lys	Val	Lys	Glu	Trp 60	Val	Ala	Ala	His
Asp 65	Gly	His	Thr	Val	Ile 70	Thr	Asn	Val	Leu	Ile 75	Ala	Asn	Asn	Gly	Ile 80
Ala	Ala	Val	Lys	Glu 85	Ile	Arg	Ser	Val	Arg 90	Lys	Trp	Ala	Tyr	Glu 95	Thr
Phe	Gly	Asp	Glu 100	Arg	Ala	Ile	Gln	Phe 105	Thr	Val	Met	Ala	Thr 110	Pro	Glu
Asp	Leu	Gln 115	Ala	Asn	Ala	Asp	Tyr 120	Ile	Arg	Met	Ala	Asp 125	His	Tyr	Val
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Ile 145	Val	Asp	Val	Ala	Glu 150	Arg	Met	Asn	Val	His 155	Ala	Val	Trp	Ala	Gly 160
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Ser	Pro	Lys	Lys 180	Ile	Ile	Phe	Ile	Gly 185	Pro	Pro	Gly	Ser	Ala 190	Met	Arg
Ser	Leu	Gly 195	Asp	Lys	Ile	Ser	Ser 200	Thr	Ile	Val	Ala	Gln 205	His	Ala	Gln
Val	Pro 210	Cys	Ile	Pro	Trp	Ser 215	_	Thr	Gly	Val	Asp 220	Ala	Val	Gln	Ile
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Cys	Val	Thr	Ser	Trp 245	Gln	Glu	Gly	Leu	Glu 250	Lys	Ala	Arg	Gln	Ile 255	Gly
Phe	Pro	Val	Met 260	Ile	Lys	Ala	Ser	Glu 265	Gly	Gly	Gly	Gly	Lys 270	Gly	Ile

Arg	Lys	Ala 275	Val	Ser	Glu	Glu	Gly 280	Phe	Glu	Glu	Leu	Tyr 285	Lys	Ala	Ala
Ala	Ser 290	Glu	Ile	Pro	Gly	Ser 295	Pro	Ile	Phe	Ile	Met 300		Leu	Ala	Gly
Asn 305	Ala	Arg	His	Leu	Glu 310	Val	Gln	Leu	Leu	Ala 315	Asp	Gln	Tyr	Gly	Asn 320
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Lys	Ala	Met 355	Glu	Glu	Ala	Ala	Val 360	Arg	Leu	Ġly	Arg	Leu 365	Val	Gly	Tyr
Val	Ser 370	Ala	Gly	Thr	Val	Glu 375	Tyr	Leu	Tyr	Ser	His 380	Ala	Asp	Asp	Lys
Phe 385	Tyr	Phe	Leu	Glu	Leu 390	Asn	Pro	Arg	Leu	Gln 395	Val	Glu	His	Pro	Thr 400
Thr	Glu	Gly	Val	Ser 405	Gly	Val	Asn	Leu	Pro 410	Ala	Ser	Gln	Leu	Gln 415	Ile
Ala	Met	Gly	Ile 420	Pro	Leu	His	Arg	Ile 425	Ser	Asp	Ile	Arg	Leu 430	Leu	Tyr
Gly	Val	Asp 435	Pro	Lys	Leu	Ser	Thr 440	Glu	Ile	Asp	Phe	Asp 445	Phe	Lys	Asn
Pro	Asp 450	Ser	Glu	Lys	Thr	Gln 455	Arg	Arg	Pro	Ser	Pro 460	Lys	Gly	His	Leu
Thr 465	Ala	Cys	Arg	Ile	Thr 470	Ser	Glu	Asp	Pro	Gly 475	Glu	Gly	Phe	Lys	Pro 480
Ser	Asn	Gly	Val	Met 485	His	Glu	Leu	Asn	Phe 490	Arg	Ser	Ser	Ser	Asn 495	Val
Trp	Gly	Tyr	Phe 500	Ser	Val	Gly	Thr	Gln 505	Gly	Gly	Ile	His	Ser 510	Phe	Ser
Asn	Ser	Gln	Phe	Glv	His	Ile	Phe	Ala	Tvr	Glv	Glu	Asn	Ara	Ser	Ala

515 520 525

Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly

	530	•				535					540					
Asp 545	Phe	Arg	Thr	Thr	Val 550	Glu	Tyr	Leu	Ile	Lys 555	Leu	Leu	Glu	Thr	Glu 560	
Ala	Phe	Glu		Asn 565	Thr	Ile	Thr	Thr	GÍy 570	Trp	Leu	Asp	Glu	Leu 575	Ile	
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	L> 1 2> 3> 2	misc_ (226) Alter elimi	(2 catio	228) on of					esult	ts in	n Sei	c to	Tyr	muta	ation	that
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ggc Gly	ctc Leu	aat Asn 35	aca Thr	gta Val	gat Asp	aaa Lys	cta Leu 40	gag Glu	gag Glu	tcc Ser	ccg Pro	tta Leu 45	agg Arg	gac Asp	ttt Phe	144
gtt Val	aag Lys 50	agt Ser	cac His	ggt Gly	ggt Gly	cac His 55	acg Thr	gtc Val	ata Ile	tcc Ser	aag Lys 60	atc Ile	ctg Leu	ata Ile	gca Ala	192
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		gag Glu														288

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	_				cca Pro											•	624
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			_		tgt Cys 230	_										•	720
_	_	_			ttt Phe		_	_								•	768
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- Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60
- Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp

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- Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125
- Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140
- Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160
- Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly
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- Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190
- Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205

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Ala	Lys	Arg	Ile	Gly 245	Phe	Pro	Val	Met	Ile 250	Lys	Ala	Ser	Glu	Gly 255	Gly
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Leu	Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met	Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala
Asp 305		Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315		Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340		His	Glu	Met	Glu 345		Ala	Ala	Val	Arg 350	Leu	Gly
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Phe	Glu	Phe 435	Lys	Thr	Gln	Asp	Ala 440	Thr	Lys	Lys	Gln	Arg 445	Arg	Pro	Ile

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460	
Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480	
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Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510	
Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525	
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				gta Val 85												288
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				cgt Arg												480
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				Gly											tta Leu	576
			Ile	gct Ala											ggc	624
		His		tct Ser											aaa Lys	672
			_	ttc Phe	_										tta Leu 240	720
				gca Ala 245												768
				agc Ser												816
_			Lys	cgt Arg				-								864
				gat Asp												912

290	295	300

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	_		_			gca Ala	_	_						_	_	1008
_		_	_	_		gga Gly						_	_		_	1056
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	_		-			ggc Gly		-		_	_				_	1536
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				_					-		tca Ser					1728
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Ala	Ala 130	Val	Lys	Cys	Met	Arg 135	Ser	Ile	Arg	Arg	Trp 140	Ser	Tyr	Glu	Met
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Asp	Leu	Lys	Ala	Asn 165	Ala	Glu	Tyr	Ile	Lys 170	Met	Ala	Asp	His	Tyr 175	Val
Pro	Val	Pro	Gly 180	Gly	Pro	Asn	Asn	Asn 185	Asn	Tyr	Ala	Asn	Val 190	Glu	Leu
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Trp	Gly 210	His	Ala	Ser	Glu	Asn 215	Pro	Lys	Leu	Pro	Glu 220	Leu	Leu	Leu	Lys
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Gly	Asp	Lys	Ile	Ala 245	Ser	Ser	Ile	Val	Ala 250	Gln	Thr	Ala	Gly	Ile 255	Pro
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Asp	Phe	Ser 275	Lys	Arg	Ile	Leu	Asn 280	Val	Pro	Gln	Glu	Leu 285	Tyr	Glu	Lys
Gly	Tyr 290				Val		Asp					Ala	Glu	Glu	Val
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- Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly 405 410 415
- Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser 420 425 430
- Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys 435 440 445
- Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile 450 455 460
- Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr 465 470 475 480
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- His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser 500 510
- Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu 515 520 525
- Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala 530 540
- Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys 555 560
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- Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu 580 585 590
- Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile 595 600 605

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														ccg Pro		96
acc Thr	aag Lys	agt Ser 35	aaa Lys	tca Ser	gaa Glu	gca Ala	aac Asn 40	ctc Leu	atc Ile	ccg Pro	agc Ser	cag Gln 45	gag Glu	ccc Pro	ttt Phe	144
cca Pro	gcc Ala 50	tct Ser	gat Asp	aac Asn	tca Ser	999 Gly 55	gag Glu	aca Thr	ccg Pro	cag Gln	aga Arg 60	aat Asn	Gly 333	gag Glu	ggc Gly	192
cac His 65	act Thr	ctg Leu	ccc Pro	aag Lys	aca Thr 70	ccc Pro	agc Ser	cag Gln	gcc Ala	gag Glu 75	cca Pro	gcc Ala	tcc Ser	cac His	aaa Lys 80	240
ggc Gly	ccc Pro	aaa Lys	gat Asp	gcc Ala 85	ggt Gly	cgg Arg	cgg Arg	aga Arg	aac Asn 90	tcc Ser	cta Leu	cca Pro	ccc Pro	tcc Ser 95	cac His	288
														ccc Pro		336
														gcc Ala		384
														caa Gln		432
						Asp								agg Arg		480

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act gga ggc ctg cac gag ttt gcg gat tcc caa ttt ggg cac tgc ttc Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe 690 695 700	2112
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acc ggg tgg ttg gac tac ctc att gct gag aaa gtg cag gag aaa ccg Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro 755 760 765	2304
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Leu	Met	Thr	Asn	Phe 165	Ile	Leu	Gly	Ser	Phe 170	Asp	Asp	Tyr	Ser	Ser 175	Asp
Glu	Asp	Ser	Val 180	Ala	Gly	Ser	Ser	Arg 185	Glu	Ser	Thr	Arg	Lys 190	Gly	Ser
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Glu	Ala 210	Glu	Thr	Arg	Val	Pro 215	Thr	Met	Arg	Pro	Ser 220	Met	Ser	Gly	Leu
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Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala 595 600 605

Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly 610 620

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Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu 655

Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu 660 670

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Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe 690 695 700

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Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp 740 745 750

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<212> DNA

<213> Homo sapiens

<220> <221> CDS <222> (1)(1596) <223> N-terminal delet	ed Human ACCasel	BC domain (AAs 1	.02-632)
<400> 13 atg gtg gct tct cca gca Met Val Ala Ser Pro Ala 1 5		_	
gtg att gag aag gtt ctt Val Ile Glu Lys Val Leu 20			_
tgc atg cgg tct atc cgt Cys Met Arg Ser Ile Arg 35		_	_
cgt gca att aga ttc gtt Arg Ala Ile Arg Phe Val 50			
aat gca gaa tac att aag Asn Ala Glu Tyr Ile Lys 65 70			
gga cca aac aac aac aac Gly Pro Asn Asn Asn 85	_	_	
gct aaa agg atc cca gtg Ala Lys Arg Ile Pro Val 100			
tct gag aat ccc aaa cta Ser Glu Asn Pro Lys Leu 115			
ttc atg ggt cct cca ago Phe Met Gly Pro Pro Ser 130			_
gca tct tcc ata gtg gct Ala Ser Ser Ile Val Ala 145 150	Gln Thr Ala Gly		
agc ggc agt ggt ctt cgt Ser Gly Ser Gly Leu Arg 165			
cgt atc tta aat gtt ccc Arg Ile Leu Asn Val Pro 180		_	_
gat gtg gat gat ggg cta Asp Val Asp Asp Gly Leu 195			
atg atc aag gcc tca gag Met Ile Lys Ala Ser Glu		_	_

210 215 220

											cag Gln					720
											gcc Ala					768
											ggc Gly					816
											cat His					864
											gta Val 300					912
											ggt Gly					960
											agc Ser					1008
											tgt Cys					1056
gct Ala	gat Asp	gtc Val 355	aat Asn	ctc Leu	cct Pro	gca Ala	gca Ala 360	cag Gln	ctc Leu	cag Gln	att Ile	gcc Ala 365	atg Met	Gly aaa	att Ile	1104
		Tyr									tat Tyr 380					1152
											gca Ala					1200
											agt Ser					1248
				Pro							gag Glu					1296
			Asn								gct Ala				gga Gly	1344
		Glu					Gln					Phe			gga Gly	1392

gaa aac aga gaa gag gca att tca aac atg gtg gtg gct ttg aag gag Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu 465 470 475 480	1440
ctg tct att cgg ggt gac ttt cga act aca gtt gaa tac ctg atc aaa Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 485 490 495	1488
ttg tta gag act gaa agc ttt cag atg aac aga att gat act ggc tgg Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp 500 505 510	1536
ctg gac aga ctg ata gca gaa aaa gta cag gct gag cga cct gac acc Leu Asp Arg Leu Ile Ala Glu Lys Val Gln Ala Glu Arg Pro Asp Thr 515 520 525	1584
atg ttg ggg gtt Met Leu Gly Val 530	1596
<210> 14 <211> 532 <212> PRT <213> Homo sapiens	
<400> 14	
Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys 1 5 10 15	
Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 20 25 30	
Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu 35 40 45	
Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60	
Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 65 70 75 80	
Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile 85 90 95	
Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110	
Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala 115 120 125	

Phe	Met 130	Gly	Pro	Pro	Ser	Gln 135	Ala	Met	Trp	Ala	Leu 140	Gly	Asp	Lys	Ile
Ala 145	Ser	Ser	Ile	Val	Ala 150	Gln	Thr	Ala	Gly	Ile 155	Pro	Thr	Leu	Pro	Trp 160
Ser	Gly	Ser	Gly	Leu 165	Arg	Val	Asp	Trp	Gln 170	Glu	Asn	Asp	Phe	Ser 175	Lys
Arg	Ile	Leu	Asn 180	Val	Pro	Gln	Glu	Leu 185	Tyr	Glu	Lys	Gly	Туг 190	Val	Lys
Asp	Val	Asp 195	Asp	Gly	Leu	Lys	Ala 200	Ala	Glu	Glu		Gly 205	Tyr	Pro	Val
Met	Ile 210	Lys	Ala	Ser	Glu	Gly 215	Gly	Ġly	Gly	Lys	Gly 220	Ile	Arg	Lys	Val
Asn 225	Asn	Ala	Asp	Asp	Phe 230	Pro	Asn	Leu	Phe	Arg 235	Gln	Val	Gln	Ala	Glu 240
Val	Pro	Gly	Ser	Pro 245	Ile	Phe	Val	Met	Arg 250		Ala	Lys	Gln	Ser 255	Arg
His	Leu	Glu	Val 260	Gln	Ile	Leu	Ala	Asp 265	Gln	Tyr	Gly	Asn	Ala 270	Ile	Ser
Leu	Phe	Gly 275	_	Asp	Cys	Ser	Val 280	Gln	Arg	Arg	His	Gln 285	Lys	Ile	Ile
Glu	Glu 290	Ala	Pro	Ala	Thr	Ile 295	Ala	Thr	Pro	Ala	Val 300	Phe	Glu	His	Met
Glu 305	Gln	Cys	Ala	Val	Lys 310	Leu	Ala	Lys	Met	Val 315		Tyr	Val	Ser	Ala 320
Gly	Thr	Val	Glu	Tyr 325	Leu	Tyr	Ser	Gln	Asp 330		Ser	Phe	Tyr	Phe 335	Leu
Glu	Leu	Asn	Pro 340	Arg	Leu	Gln	Val	Glu 345	His	Pro	Cys	Thr	Glu 350	Met	Val
Ala	Asp	Val 355	Asn	Leu	Pro	Ala	Ala 360	Gln	Leu	Gln	Ile	Ala 365	Met	Gly	Ile
Pro	Leu	Tvr	Ara	Ile	Lvs	Asp	Ile	Ara	Met	Met	Tvr	Glv	Val	Ser	Pro

370 375 380

Trp 385	Gly	Asp	Ser	Pro	Ile 390	Asp	Phe	Glu	Asp	Ser 395	Ala	His	Val	Pro	Cys 400		
Pro	Arg	Gly	His	Val 405	Ile	Ala	Ala	Arg	Ile 410	Thr	Ser	Glu	Asn	Pro 415	Asp		
Glu	Gly	Phe	Lys 420	Pro	Ser	Ser	Gly	Thr 425	Val	Gln	Glu	Leu	Asn 430	Phe	Arg		
Ser	Asn	Lys 435	Asn	Val	Trp	Gly	Tyr 440	Phe	Ser	Val	Ala	Ala 445	Ala	Gly	Gly		
Leu	His 450	Glu	Phe	Ala	Asp	Ser 455	Gln	Phe	Gly	His	Cys 460	Phe	Ser	Trp	Gly		
Glu 465	Asn	Arg	Glu	Glu	Ala 470	Ile	Ser	Asn	Met	Val 475	Val	Ala	Leu	Lys	Glu 480		
Leu	Ser	Ile	Arg	Gly 485	Asp	Phe	Arg	Thr	Thr 490	Val	Glu	Tyr	Leu	Ile 495	Lys		
Leu	Leu	Glu	Thr 500	Glu	Ser	Phe	Gln	Met 505	Asn	Arg	Ile	Asp	Thr 510	Gly	Trp		
		Arg 515		Ile	Ala	Glu	Lys 520	Val	Gln	Ala	Glu	Arg 525	Pro	Asp	Thr		
	530		Val														
<21	1> 2>	15 1596 DNA Homo	sap:	iens													
<22	1> 2>	CDS (1). N-te:	-		elet	ed Hi	ıman	ACC	ase2	BC (doma:	in (AAs 2	244-	774)		
atg		15 gct Ala			_											4	8
_		gag Glu	_	_												9	6

_		_				•		gcc Ala		_	_		-			144
								gtg Val								192
								gat Asp							_	240
								aac Asn								288
								gtg Val 105							_	336
	_					_		ctg Leu	_	_	_			_	_	384
								atg Met						_		432
								cta Leu								480
								tgg Trp								528
								gat Asp 185	_		_	_		_		576
								gca Ala								624
_	_			_		_		ggc Gly			_				_	672
_		_			_		_	atc Ile			_		_	_	_	720
				_				ctc Leu	_	_	_	-	_		_	768
		=	-	_				gct Ala 265	_	-				_		816

	_								cag Gln							864
_		_	-						ccg Pro							912
_	_	_	-	_				_	aag Lys	_				_		960
_				_					cag Gln 330							1008
_	_	_							gaa Glu							1056
	-	_	_						cag Gln			_	_		_	1104
		_			_				cgg Arg							1152
									gaa Glu							1200
	_	_			_		-	_	aga Arg 410			_				1248
_				_	_	_			act Thr	_	_	_				1296
									ttc Phe							1344
									ttt Phe							1392
						_			aac Asn							1440
_									act Thr 490							1488
		_			_	_		_	aac Asn		_					1536

.

tgg ttg gac tac ctc att gct gag aaa gtg cag gag aaa ccg gat atc Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro Asp Ile 515 520 525	1584
atg ctt ggg gtg Met Leu Gly Val 530	1596
<210> 16 <211> 532 <212> PRT <213> Homo sapiens	
<400> 16	
Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg 1 5 10 15	
Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 20 25 30	
Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu 35 40 45	
Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60	
Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 65 70 75 80	
Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile 85 90 95	
Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110	
Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala 115 120 125	
Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile 130 135 140	
Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg 145 150 155 160	
Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln 165 170 175	

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val

Lys	Asp	Val 195	Asp	Glu	Gly	Leu	Glu 200	Ala	Ala	Glu	Arg	Ile 205	Gly	Phe	Pro
Leu	Met 210	Ile	Lys	Ala	Ser	Glu 215	Gly	Gly	Gly	Gly	Lys 220	Gly	Ile	Arg	Lys
Ala 225	Glu	Ser	Ala	Glu	Asp 230	Phe	Pro	Ile	Leu	Phe 235	Arg	Gln	Val	Gln	Ser 240
Glu	Ile	Pro	Gly	Ser 245	Pro	Ile	Phe	Leu	Met 250	Lys	Leu	Ala	Gln	His 255	Ala
Arg	His	Leu	Glu	Val	Gln	Ile	Leu	Ala	Asp	Gln	Tyr	Gly	Asn	Ala	Val

Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile

Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe

Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser

Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe

Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met

Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser

Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro

Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro

Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe

Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly
435
440
445

Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp
450 460

Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys 465 470 475 480

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 485 490 495

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly 500 505 510

Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val Gln Glu Lys Pro Asp Ile 515 520 525

Met Leu Gly Val 530

<210> 17

<211> 554

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC_FEATURE

<222> (1)..(554)

<223> N-terminal deleted Ustilago ACCase BC domain (AAs 7-560)

<400> 17

Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro 1 10 15

Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val 20 25 30

Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu 35 40 45

Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg 50 55 60

Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn 65 70 75 80

Ala	Asp	Tyr	Ile	Arg 85	Met	Ala	Asp	Gln	Tyr 90	Val	Glu	Val	Pro	Gly 95	Gly
Ser	Asn	Asn	Asn 100	Asn	Tyr	Ala	Asn	Val 105	Asp	Leu	Ile	Val	Asp 110	Val	Ala
Glu	Arg	Ala 115	Gly	Val	His	Ala	Val 120	Trp	Ala	Gly	Trp	Gly 125	His	Ala	Ser
Glu	Asn 130	Pro	Arg	Leu	Pro	Glu 135	Ser	Leu	Ala	Ala	Ser 140	Lys	His	Lys	Ile
Ile 145	Phe	Ile	Gly	Pro	Pro 150	Gly	Ser	Ala	Met	Arg 155	Ser	Leu	Gly	Asp	Lys 160
Ile	Ser	Ser	Thr	Ile 165	Val	Ala	Gln	His	Ala 170	Asp	Val	Pro	Cys	Met 175	Pro
Trp	Ser	Gly	Thr 180	Gly	Ile	Lys	Glu	Thr 185	Met	Met	Ser	Asp	Gln 190	Gly	Phe
Leu	Thr	Val 195	Ser	Asp	Asp	Val	Tyr 200		Gln	Ala	Cys	Ile 205	His	Thr	Ala
Glu	Glu 210		Leu	Glu	Lys	Ala 215	Glu	Lys	Ile	Gly	Tyr 220	Pro	Val	Met	Ile
Lys 225		Ser	Glu	Gly	Gly 230	Gly	Gly	Lys	Gly	Ile 235		Lys	Cys	Thr	Asn 240
Gly	Glu	Glu	Phe	Lys 245	Gln	Leu	Tyr	Asn	Ala 250		Leu	Gly	Glu	Val 255	
_		Pro			Val										Leu
Glu	Val	Gln 275		Leu	Ala	Asp	Gln 280	Tyr	Gly	Asn	Ala	Ile 285		Ile	Phe
Gly	Arg 290		Cys	Ser	Val	Gln 295		Arg	His	Gln	Lys 300		Ile	Glu	Glu
Ala 305		Val	Thr	Ile	Ala 310		Glu	Asp	Ala	Arg 315		Ser	Met	Glu	Lys 320

Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn

Ala Glu Arg Pro Pro Ala Asp Leu Ala Val 545 550

Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr

- <210> 18
- <211> 549
- <212> PRT
- <213> Ustilago maydis
- <220>
- <221> MISC_FEATURE
- <222> (1)..(549)
- <223> N-terminal deleted Ustilago ACCase BC domain (AAs 12-560)
- <400> 18
- Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala 1 5 10 15
- Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu 20 25 30
- Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg 35 40 45
- Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr 50 55 60
- Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg 65 70 75 80
- Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn 85 90 95
- Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val
 100 105 110
- His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu 115 120 125
- Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro 130 135 140
- Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile 145 150 155 160
- Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly
 165 170 175
- Ile Lys Glu Thr Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp 180 185 190

Asp Val Tyr 195	Gln Gln	Ala Cys	Ile H 200	His Thr	Ala	Glu	Glu 205	Gly	Leu	Glu
Lys Ala Glu 210	Lys Ile	Gly Tyr 215		Val Met	Ile	Lys 220	Ala	Ser	Glu	Gly
Gly Gly Gly 225	Lys Gly	Ile Arg 230	Lys (Cys Thr	Asn 235	Gly	Glu	Glu	Phe	Lys 240
Gln Leu Tyr	Asn Ala 245	Val Leu	Gly (Glu Val 250		Gly	Ser	Pro	Val 255	Phe
Val Met Lys	Leu Ala 260	Gly Gln		Arg His 265	Leu	Glu	Val	Gln 270	Leu	Leu
Ala Asp Gln 275	Tyr Gly	Asn Ala	Ile 8 280	Ser Ile	Phe	Gly	Arg 285	Asp	Cys	Ser
Val Gln Arg 290	Arg His	Gln Lys 295		Ile Glu	Glu	Ala 300	Pro	Val	Thr	Ile
Ala Pro Glu 305	Asp Ala	Arg Glu 310	Ser N	Met Glu	. Lys 315	Ala	Ala	Val	Arg	Leu 320
Ala Lys Leu	Val Gly 325	_	Ser A	Ala Gly 330		Val	Glu	Trp	Leu 335	Tyr
Ser Pro Glu	Ser Gly 340	Glu Phe		Phe Leu 345	Glu	Leu	Asn	Pro 350	Arg	Leu
Gln Val Glu 355	His Pro	Thr Thr	Glu N 360	Met Val	Ser	Gly	Val 365	Asn	Ile	Pro
Ala Ala Gln 370	Leu Gln	Val Ala 375		Gly Ile	Pro	Leu 380	Tyr	Ser	Ile	Arg
Asp Ile Arg 385	Thr Leu	Tyr Gly 390	Met A	Asp Pro	Arg 395	Gly	Asn	Glu	Val	Ile 400
Asp Phe Asp	Phe Ser 405	Ser Pro	Glu S	Ser Phe 410	_	Thr	Gln	Arg	Lys 415	Pro
Gln Pro Gln	Gly His 420	Val Val		Cys Arg 425	Ile	Thr	Ala	Glu 430	Asn	Pro
Asp Thr Gly	Phe Lys	Pro Gly	Met (Gly Ala	Leu	Thr	Glu	Leu	Asn	Phe

435 440 445

Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly 450 455 460

Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr 465 470 475 480

Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys 485 490 495

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 500 505 510

Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly 515 520 525

Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro 530 540

Ala Asp Leu Ala Val 545

<210> 19

<211> 539

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC FEATURE

<222> (1)..(539)

<223> N-terminal deleted Ustilago ACCse BC domain (AAs 22-560)

<400> 19

Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser 1 5 10 15

Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys 20 25 30

Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu
35 40 45

Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val 50 60

Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly

Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val 85 90 95

Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110

Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys 115 120 125

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp 130 135 140

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met 145 150 155 160

Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly 165 170 175

Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr 180 185 190

Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met 195 200 205

Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Cys Thr 210 215 220

Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly Glu Val 225 230 235 240

Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala Arg His 245 250 255

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile Ser Ile 260 265 270

Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu 275 280 285

Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser Met Glu 290 295 300

Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser Ala Gly 305 310 315 320

Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala Phe Leu
325 330 335

Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val
340 345 350

Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile 355 360 365

Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro 370 375 380

Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe 385 390 395 400

Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg 405 410 415

Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala 420 425 430

Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe 435 440 445

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe 450 455 460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln 465 470 475 480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr 485 490 495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser 500 510

Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu 515 520 525

Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala Val 530 535

<210> 20

<211> 529

<212> PRT

- <213> Ustilago maydis
- <220>
- <221> MISC FEATURE
- <222> (1)..(529)
- <223> N-terminal deleted Ustilago ACCase BC domain (AAs 32-560)
- <400> 20
- Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn 1 5 10 15
- Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr
 20 25 30
- Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr 35 40 45
- Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln 50 55
- Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val 65 70 75 80
- Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp
 85 90 95
- Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu 100 105 110
- Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala 115 120 125
- Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His 130 135 140
- Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr 145 150 155 160
- Met Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln
 165 170 175
- Gln Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys 180 185 190
- Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys 195 200 205

Gly	11e 210	Arg	Lys	Cys	Thr	Asn 215	Gly	Glu	Glu	Phe	Lys 220	Gln	Leu	Tyr	Asn
Ala 225	Val	Leu	Gly	Glu	Val 230	Pro	Gly	Ser	Pro	Val 235	Phe	Val	Met	Lys	Leu 240
Ala	Gly	Gln	Ala	Arg 245	His	Leu	Glu	Val	Gln 250	Leu	Leu	Ala	Asp	Gln 255	Tyr
Gly	Asn	Ala	Ile 260	Ser	Ile	Phe	Gly	Arg 265	Asp	Cys	Ser	Val	Gln 270	Arg	Arg
His	Gln	Lys 275	Ile	Ile	Glu	Glu	Ala 280	Pro	Val	Thr	Ile	Ala 285	Pro	Glu	Asp
Ala	Arg 290	Glu	Ser	Met	Glu	Lys 295	Ala	Ala	Val	Arg	Leu 300	Ala	Lys	Leu	Val
Gly 305	Tyr	Val	Ser	Ala	Gly 310	Thr	Val	Glu	Trp	Leu 315	Tyr	Ser	Pro	Glu	Ser 320
Gly	Glu	Phe	Ala	Phe 325	Leu	Glu	Leu	Asn	Pro 330	Arg	Leu	Gln	Val	Glu 335	His
Pro	Thr	Thr	Glu 340	Met	Val	Ser	Gly	Val 345	Asn	Ile	Pro	Ala	Ala 350	Gln	Leu
Gln	Val	Ala 355	Met	Gly	Ile	Pro	Leu 360	Tyr	Ser	Ile	Arg	Asp 365	Ile	Arg	Thr
Leu	Tyr 370	Gly	Met	Asp	Pro	Arg 375	Gly	Asn	Glu	Val	Ile 380	Asp	Phe	Asp	Phe
Ser 385	Ser	Pro	Glu	Ser	Phe 390		Thr			Lys 395			Pro		Gly 400
His	Val	Val	Ala	Cys 405	Arg	Ile	Thr	Ala	Glu 410	Asn	Pro	Asp	Thr	Gly 415	Phe
Lys	Pro	Gly	Met 420	Gly	Ala	Leu	Thr	Glu 425	Leu	Asn	Phe	Arg	Ser 430	Ser	Thr
Ser	Thr	Trp 435	Gly	Tyr	Phe	Ser	Val 440	Gly	Thr	Ser	Gly	Ala 445	Leu	His	Glu

Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp Leu Ala Val <210> <211> <212> PRT<213> Ustilago maydis <220> <221> MISC FEATURE (1)..(519)<222> N-terminal deleted Ustilago ACCase BC domain (AAs 42-560) <223> <400> 21 Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala

Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro

Arg L	Leu	Pro	Glu 100	Ser	Leu	Ala	Ala	Ser 105	Lys	His	Lys	Ile	Ile 110	Phe	Ile
Gly F		Pro 115	Gly	Ser	Ala	Met	Arg 120	Ser	Leu	Gly	Asp	Lys 125	Ile	Ser	Ser
Thr I	le 130	Val	Ala	Gln	His	Ala 135	Asp	Val	Pro	Cys	Met 140	Pro	Trp	Ser	Gly
Thr G 145	Sly	Ile	Lys	Glu	Thr 150	Met	Met	Ser	Asp	Gln 155	Gly	Phe	Leu	Thr	Val 160
Ser A	4sp	Asp	Val	Tyr 165	Gln	Gln	Ala	Cys	Ile 170	His	Thr	Ala	Glu	Glu 175	Gly
Leu G	lù	Lys	Ala 180	Glu	Lys	Ile	Gly	Tyr 185	Pro	Val	Met	Ile	Lys 190	Ala	Ser
Glu G	_	Gly 195	Gly	Gly	Lys	Gly	Ile 200	Arg	Lys	Cys	Thr	Asn 205	Gly	Glu	Glu
Phe I	Ув 210	Gln	Leu	Tyr	Asn	Ala 215	Val	Leu	Gly	Glu	Val 220	Pro	Gly	Ser	Pro
Val F 225	Phe	Val	Met	Lys	Leu 230	Ala	Gly	Gln	Ala	Arg 235	His	Leu	Glu	Val	Gln 240
Leu I	Leu	Ala	Asp	Gln 245	Tyr	Gly	Asn	Ala	Ile 250	Ser	Ile	Phe	Gly	Arg 255	Asp
Cys S	Ser	Val	Gln 260	Arg	Arg	His	Gln	Lys 265	Ile	Ile	Glu	Glu	Ala 270	Pro	Val
Thr I		Ala 275	Pro	Glu	Asp	Ala	Arg 280	Glu	Ser	Met	Glu	Lys 285	Ala	Ala	Val
Arg I	Leu 290	Ala	Lys	Leu	Val	Gly 295	Tyr	Val	Ser	Ala	Gly 300	Thr	Val	Glu	Trp
Leu 1	fyr	Ser	Pro	Glu	Ser 310	Gly	Glu	Phe	Ala	Phe 315	Leu	Glu	Leu	Asn	Pro 320
Arg I	Leu	Gln	Val	Glu 325	His	Pro	Thr	Thr	Glu 330	Met	Val	Ser	Gly	Val 335	Asn
Ile F	Pro	Ala	Ala	Gln	Leu	Gln	Val	Ala	Met	Gly	Ile	Pro	Leu	Tyr	Ser

340 345 350

Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met Asp Pro Arg Gly Asn Glu 355 360 365

Val Ile Asp Phe Asp Phe Ser Ser Pro Glu Ser Phe Lys Thr Gln Arg 370 375 380

Lys Pro Gln Pro Gln Gly His Val Val Ala Cys Arg Ile Thr Ala Glu 385 390 395 400

Asn Pro Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu 405 410 415

Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr 420 425 430

Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe 435 440 / 445

Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser 450 460

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr 465 470 475 480

Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr 485 490 495

Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr Ala Glu Arg 500 505 510

Pro Pro Ala Asp Leu Ala Val 515

<210> 22

<211> 554

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC FEATURE

<222> (1)..(554)

<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-555)

<400> 22

Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro

1

5

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln 20 25 30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 35 40 45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 50 60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu 65 70 75 80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val 85 90 95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly 115 120 125

Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala 130 135 140

Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg 145 150 155 160

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp 165 170 175

Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met 180 185 190

Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala 195 200 205

Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly 210 220

Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile 225 230 235 240

Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val 245 250 255

Leu	GIY	GIU	260	Pro	GIA	ser	Pro	265	Pile	vai	Mec	БУБ	270	AIA	GIY
Gln	Ala	Arg 275	His	Leu	Glu	Val	Gln 280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala	Ile 290	Ser	Ile	Phe	Gly	Arg 295	Asp	Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys 305	Ile	Ile	Glu	Glu	Ala 310	Pro	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu	Ser	Met	Glu	Lys 325	Ala	Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val	Ser	Ala	Gly 340	Thr	Val	Glu	Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350	Gly	Glu
Phe	Ala	Phe 355		Glu	Leu	Asn	Pro 360	Arg	Leu	Gln	Val	Glu 365	His	Pro	Thr
Thr	Glu 370		Val	Ser	Gly	Val 375		Ile	Pro	Ala	Ala 380	Gln	Leu	Gln	Val
Ala 385	Met	Gly	Ile	Pro	Leu 390		Ser	Ile	Arg	Asp 395		Arg	Thr	Leu	Tyr 400
Gly	Met	Asp	Pro	Arg 405	Gly	Asn	Glu	Val	Ile 410		Phe	Asp	Phe	Ser 415	Ser
Pro	Glu	Ser	Phe 420		Thr	Gln	Arg	Lys 425		Gln	Pro	Gln	Gly 430	His	Val
Val	Ala	Cys 435	-	Ile	Thr	Ala	Glu 440		Pro	Asp	Thr	Gly 445		Lys	Pro
Gly	Met 450		Ala	Leu	Thr	Glu 455		Asn	Phe	Arg	Ser 460		Thr	Ser	Thr
Trp 465	_	Tyr	Phe	Ser	Val 470		Thr	Ser	Gly	Ala 475		His	Glu	Tyr	Ala 480
Asp	Ser	Gln	. Phe	Gly 485	His	Ile	Phe	Ala	Tyr 490		Ala	Asp	Arg	Ser 495	

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
500 505 510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp 515 520 525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile 530 540

Gln Asp Arg Leu Thr Ala Glu Arg Pro Pro 545

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<211> 549

<212> PRT

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<220>

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<222> (1)..(549)

<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-550)

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Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro 1 5 10 15

Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln
20 25 30

Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 35 40 45

Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 50 60

Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu 65 70 75 80

Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val 85 90 95

Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110

Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly 115 120 125

Trp	Gly 130	His	Ala	Ser	GIu	Asn 135	Pro	Arg	Leu	Pro	140	ser	Leu	Ala	Ald
Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	His	Ala 175	Asp
Val	Pro	Cys	Met 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Ile	Lys	Glu	Thr 190	Met	Met
Ser	Asp	Gln 195	Gly	Phe	Leu	Thr	Val 200	Ser	Asp	Asp	Val	Tyr 205	Gln	Gln	Ala
Cys	Ile 210	His	Thr	Ala	Glu	Glu 215	Gly	Leu	Glu	Lys	Ala 220	Glu	Lys	Ile	Gly
Tyr 225	Pro	Val	Met	Ile	Lys 230	Ala	Ser	Glu	Gly	Gly 235	Gly	Gly	Lys	Gly	Ile 240
Arg	Lys	Cys	Thr	Asn 245	Gly	Glu	Glu	Phe	Lys 250	Gln	Leu	Tyr	Asn	Ala 255	Val
Leu	Gly	Glu	Val 260	Pro	Gly	Ser	Pro	Val 265	Phe	Val	Met	Lys	Leu 270	Ala	Gly
Gln	Ala	Arg 275	His	Leu	Glu	Val	Gln 280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala	Ile 290		Ile	Phe	Gly	Arg 295		Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys 305		Ile	Glu	Glu	Ala 310	Pro	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu	Ser	Met	Glu	Lys 325	Ala	Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val	Ser	Ala	Gly 340	Thr	Val	Glu	Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350		Glu
Phe	Ala	Phe		Glu	Leu	Asn	Pro 360	Arg	Leu	Gln	Val	Glu 365		Pro	Thr

Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val 370 375 380

Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr 385 390 395 400

Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser 405 410 415

Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
420 425 430

Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro 435 440 445

Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr 450 460

Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala 465 470 475 480

Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu 485 490 495

Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly 500 505 510

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp 515 520 525

Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile 530 540

Gln Asp Arg Leu Thr 545

<210> 24

<211> 539

<212> PRT

<213> Ustilago maydis

<220>

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<222> (1)..(539)

<223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-540)

<400> 24

Pro 1	Pro	Pro	Asp	His 5	Lys	Ala	Val	Ser	Gln 10	Phe	Ile	Gly	Gly	Asn 15	Pro
Leu	Glu	Thr	Ala 20	Pro	Ala	Ser	Pro	Val 25	Ala	Asp	Phe	Ile	Arg 30	Lys	Gln
Gly	Gly	His 35	Ser	Val	Ile	Thr	Lys 40	Val	Leu	Ile	Cys	Asn 45	Asn	Gly	Ile
Ala	Ala 50	Val	Lys	Glu	Ile	Arg 55	Ser	Ile	Arg	Lys	Trp 60	Ala	Tyr	Glu	Thr
Phe 65	Gly	Asp	Glu	Arg	Ala 70	Ile	Glu	Phe	Thr	Val 75	Met	Ala	Thr	Pro	Glu 80
Asp	Leu	Lys	Val	Asn 85	Ala	Asp	Tyr	Ile	Arg 90	Met	Ala	Asp	Gln	Tyr 95	Val
Glu	Val	Pro	Gly 100	Gly	Ser	Asn	Asn	Asn 105	Asn	Tyr	Ala	Asn	Val 110	Asp	Leu
Ile	Val	Asp 115	Val	Ala	Glu	Arg	Ala 120	Gly	Val	His	Ala	Val 125	Trp	Ala	Gly
Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Arg	Leu	Pro	Glu 140	Ser	Leu	Ala	Ala
Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	His	Ala 175	Asp
Val	Pro	Cys	Met 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Ile	Lys	Glu	Thr 190	Met	Met
Ser	Asp	Gln 195	Gly	Phe	Leu	Thr	Val 200	Ser	Asp	Asp	Val	Tyr 205	Gln	Gln	Ala
Cys	Ile 210	His	Thr	Ala	Glu	Glu 215	Gly	Leu	Glu	Lys	Ala 220	Glu	Lys	Ile	Gly
Tyr 225	Pro	Val	Met	Ile	Lys 230	Ala	Ser	Glu	Gly	Gly 235	Gly	Gly	Lys	Gly	Ile 240
Arg	Lys	Cys	Thr	Asn	Gly	Glu	Glu	Phe	Lys	Gln	Leu	Tyr	Asn	Ala	Val

250

255

Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly 260 265 270

- Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn 275 280 285
- Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln 290 295 300
- Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg 305 310 315 320
- Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr 325 330 335
- Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu 340 345 350
- Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr 355 360 365
- Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val 370 375 380
- Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr 385 390 395 400
- Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser 405 410 415
- Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val 420 425 430
- Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro 435 440 445
- Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr 450 460
- Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala 465 470 475 480
- Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu 485 490 495

- Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly 500 505 510
- Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp 515 520 525
- Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp 530 535
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- <211> 529
- <212> PRT
- <213> Ustilago maydis
- <220>
- <221> MISC FEATURE
- <222> (1)..(529)
- <223> C-terminal deleted Ustilago ACCase BC domain (AAs 2-530)
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- Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro 1 5 10 15
- Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln 20 25 30
- Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile 35 40 45
- Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr 50 60
- Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu 65 70 75 80
- Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val 85 90 95
- Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110
- Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly
 115 120 125
- Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala 130 135 140

Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	His	Ala 175	Asp
Val	Pro	Cys	Met 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Ile	Lys	Glu	Thr 190	Met	Met
Ser	Asp	Gln 195	Gly	Phe	Leu	Thr	Val 200	Ser	Asp	Asp	Val	Tyr 205	Gln	Gln	Ala
Cys	Ile 210	His	Thr	Ala	Glu	Glu 215	Gly	Leu	Glu	Lys	Ala 220	Glu	Lys	Ile	Gly
Tyr 225	Pro	Val	Met	Ile	Lys 230	Ala	Ser	Glu	Gly	Gly 235	Gly	Gly	Lys	Gly	Ile 240
Arg	Lys	Cys	Thr	Asn 245	Gly	Glu	Glu	Phe	Lys 250	Gln	Leu	Tyr	Asn	Ala 255	Val
Leu	Gly	Glu	Val 260	Pro	Gly	Ser	Pro	Val 265	Phe	Val	Met	Lys	Leu 270	Ala	Gly
Gln	Ala	Arg 275	His	Leu	Glu	Val	Gln 280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala	Ile 290	Ser	Ile	Phe	Gly	Arg 295	Asp	Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys 305	Ile	Ile	Glu	Glu	Ala 310	Pro	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu	Ser	Met	Glu	Lys 325	Ala	Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val	Ser	Ala	Gly 340	Thr	Val	Glu	Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350	Gly	Glu
Phe	Ala	Phe 355	Leu	Glu	Leu	Asn	Pro 360	Arg	Leu	Gln	Val	Glu 365	His	Pro	Thr
Thr	Glu 370	Met	Val	Ser	Gly	Val 375	Asn	Ile	Pro	Ala	Ala 380	Gln	Leu	Gln	Val

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Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr
385
                     390
                                          395
                                                              400
Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser
                 405
                                     410
                                                          415
Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val
             420
                                 425
                                                      430
Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro
         435
                             440
                                                  445
Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr
    450
                         455
                                              460
Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala
465
                     470
                                         475
                                                              480
Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu
                 485
                                     490
                                                          495
Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly
            500
                                 505
                                                      510
Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp
        515
                             520
                                                  525
Ala
<210>
       26
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<220>
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<222>
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<223>
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       26
Pro Pro Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro
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Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln

Gly	Gly	His 35	Ser	Val	Ile	Thr	Lys 40	Val	Leu	Ile	Cys	Asn 45	Asn	Gly	Ile
Ala	Ala 50	Val	Lys	Glu	Ile	Arg 55	Ser	Ile	Arg	Lys	Trp 60	Ala	Tyr	Glu	Thr
Phe 65	Gly	Asp	Glu	Arg	Ala 70	Ile	Glu	Phe	Thr	Val 75	Met	Ala	Thr	Pro	Glu 80
Asp	Leu	Lys	Val	Asn 85	Ala	Asp	Tyr	Ile	Arg 90	Met	Ala	Asp	Gln	Tyr 95	Val
Glu	Val	Pro	Gly 100	Gly	Ser	Asn	Asn	Asn 105	Asn	Tyr	Ala	Asn	Val 110	Asp	Leu
Ile	Val	Asp 115	Val	Ala	Glu	Arg	Ala 120	Gly	Val	His	Ala	Val 125	Trp	Ala	Gly
Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Arg	Leu	Pro	Glu 140	Ser	Leu	Ala	Ala
Ser 145	Lys	His	Lys	Ile	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Ser	Ala	Met	Arg 160
			Asp	165					170					175	
			Met 180					185					190		
		195	Gly				200					205			
-	210		Thr			215					220				
225			Met		230					235				_	240
_	-	-	Thr	245	_				250					255	
Leu	Gly	Glu	Val 260	Pro	Gly	Ser	Pro	Val 265	Phe	Val	Met	Lys	Leu 270	Ala	Gly

Gln A	la Arg 275		Leu	Glu	Val	Gln 280	Leu	Leu	Ala	Asp	Gln 285	Tyr	Gly	Asn
Ala II 29	le Ser 90	lle	Phe	Gly	Arg 295	Asp	Cys	Ser	Val	Gln 300	Arg	Arg	His	Gln
Lys I] 305	le Ile	e Glu	Glu	Ala 310	Pro	Val	Thr	Ile	Ala 315	Pro	Glu	Asp	Ala	Arg 320
Glu Se	er Met	: Glu	Lys 325	Ala	Ala	Val	Arg	Leu 330	Ala	Lys	Leu	Val	Gly 335	Tyr
Val Se	er Ala	340	Thr	Val	Glu	Trp	Leu 345	Tyr	Ser	Pro	Glu	Ser 350	Gly	Glu
Phe Al	la Phe 355		Glu	Leu	Asn	Pro 360	Arg	Leu	Gln	Val	Glu 365	His	Pro	Thr
Thr Gl	lu Met 70	: Val	Ser	Gly	Val 375	Asn	Ile	Pro	Ala	Ala 380	Gln	Leu	Gln	Val
Ala Me	et Gly	, Ile	Pro	Leu 390	Tyr	Ser	Ile	Arg	Asp 395	Ile	Arg	Thr	Leu	Tyr 400
Gly Me	et Asp	Pro	Arg 405	Gly	Asn	Glu	Val	Ile 410	Asp	Phe	Asp	Phe	Ser 415	Ser
Pro G	lu Ser	Phe 420	Lys	Thr	Gln	Arg	Lys 425	Pro	Gln	Pro	Gln	Gly 430	His	Val
Val Al	la Cys 435		Ile	Thr	Ala	Glu 440	Asn	Pro	Asp	Thr	Gly 445	Phe	Lys	Pro
Gly Me	_								_			Thr	Ser	Thr
Trp G] 465	ly Tyr	Phe	Ser	Val 470	Gly	Thr	Ser	Gly	Ala 475	Leu	His	Glu	Tyr	Ala 480
Asp Se	er Glr	Phe	Gly 485	His	Ile	Phe	Ala	Tyr 490	Gly	Ala	Asp	Arg	Ser 495	Glu
Ala Ar	rg Lys	Gln 500	Met	Val	Ile	Ser	Leu 505	Lys	Glu	Leu	Ser	Ile 510	Arg	Gly
Asp Ph	ne Arg	Thr	Thr	Val	Glu									

- <210> <211> <212> PRT <220> <221> <222> <223> <400>
- <213> Ustilago maydis
- MISC FEATURE
- (1)..(554)
- N- and C-terminal deleted Ustilago ACCase BC domain (AAs 4-547)
- Pro Asp His Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu
- Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly
- His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala
- Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly
- Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu
- Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val
- Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val
- Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly
- His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys
- His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu
- Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro
- Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp

180	185	190

- Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile 195 200 205
- His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro 210 215 220
- Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys 225 230 235 240
- Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala Val Leu Gly
 245 250 255
- Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala Gly Gln Ala 260 265 270
- Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Ala Ile 275 280 285
- Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile 290 295 300
- Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala Arg Glu Ser 305 310 315 320
- Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly Tyr Val Ser 325 330 335
- Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly Glu Phe Ala 340 345 350
- Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu 355 360 365
- Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln Val Ala Met 370 380
- Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu Tyr Gly Met 385 390 395 400
- Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser Ser Pro Glu 405 410 415
- Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His Val Val Ala 420 425 430

Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys Pro Gly Met 440 445 435 Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser Thr Trp Gly 450 460 455 Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser 470 465 475 480 Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg 485 490 495 Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 500 505 510 Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe 515 520 525 Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu Ile Gln Asp 530 535 540 Arg Leu Thr Ala Glu Arg Pro Pro Ala Asp 545 550 <210> 28 <211> 549 <212> PRT Ustilago maydis <213> <220> <221> MISC FEATURE <222> (1)..(549)N- and C-terminal deleted Ustilago ACCase BC domain (AAs 7-555) <223> <400> 28 Lys Ala Val Ser Gln Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro 10 15 Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val 20 30 25 Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu 35 40 45 Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg

60

55

Ala Ile Gl	ı Phe Thr	Val Met 70	Ala T	Thr Pro	Glu Asp 75	Leu L	ys Val	Asn 80
Ala Asp Ty	r Ile Arg 85	Met Ala	Asp G	Gln Tyr 90	Val Glu	Val P	ro Gly 95	Gly
Ser Asn As	n Asn Asn 100	Tyr Ala		Val Asp 105	Leu Ile		sp Val 10	Ala
Glu Arg Al	_	His Ala	Val 1	Trp Ala	Gly Trp	Gly H 125	is Ala	Ser
Glu Asn Pr	o Arg Leu	Pro Glu 135		Leu Ala	Ala Ser 140	Lys H	is Lys	Ile
Ile Phe Il	e Gly Pro	Pro Gly 150	Ser A	Ala Met	Arg Ser 155	Leu G	ly Asp	Lys 160
Ile Ser Se	r Thr Ile 165		Gln H	His Ala 170	Asp Val	Pro C	ys Met 175	Pro
Trp Ser Gl	y Thr Gly 180	lle Lys		Thr Met 185	Met Ser	-	ln Gly 90	Phe
Leu Thr Va		Asp Val	Tyr 0	Gln Gln	Ala Cys	Ile H 205	is Thr	Ala
Glu Glu Gl 210	y Leu Glu	Lys Ala 215		Lys Ile	Gly Tyr 220	Pro V	al Met	Ile
Lys Ala Se 225	c Glu Gly	Gly Gly 230	Gly I	Lys Gly	Ile Arg 235	Lys C	ys Thr	Asn 240
Gly Glu Gl	_	Gln Leu	_			_		Pro
Gly Ser Pro	Val Phe 260	Val Met		Leu Ala 265	Gly Gln		rg His 70	Leu
Glu Val Gla 27		Ala Asp	Gln T 280	Tyr Gly	Asn Ala	Ile Se 285	er Ile	Phe
Gly Arg As 290	Cys Ser	Val Gln 295	_	Arg His	Gln Lys 300	Ile I	le Glu	Glu

Ala 305	Pro	Val	Thr	Ile	Ala 310	Pro	Glu	Asp	Ala	Arg 315	Glu	Ser	Met	Glu	Lys 320
Ala	Ala	Val	Arg	Leu 325	Ala	Lys	Leu	Val	Gly 330	Tyr	Val	Ser	Ala	Gly 335	Thr
Val	Glu	Trp	Leu 340	Tyr	Ser	Pro	Glu	Ser 345	Gly	Glu	Phe	Ala	Phe 350	Leu	Glu
Leu	Asn	Pro 355	Arg	Leu	Gln	Val	Glu 360	His	Pro	Thr	Thr	Glu 365	Met	Val	Ser
Gly	Val 370	Asn	Ile	Pro	Ala	Ala 375	Gln	Leu	Gln	Val	Ala 380	Met	Gly	Ile	Pro
Leu 385	Tyr	Ser	Ile	Arg	Asp 390	Ile	Arg	Thr	Leu	Tyr 395	Gly	Met	Asp	Pro	Arg 400
Gly	Asn	Glu	Val	Ile 405	Asp	Phe	Asp	Phe	Ser 410	Ser	Pro	Glu	Ser	Phe 415	Lys
Thr	Gln	Arg	Lys 420	Pro	Gln	Pro	Gln	Gly 425	His	Val	Val	Ala	Cys 430	Arg	Ile
Thr	Ala	Glu 435	Asn	Pro	Asp	Thr	Gly 440	Phe	Lys	Pro	Gly	Met 445	Gly	Ala	Leu
Thr	Glu 450	Leu	Asn	Phe	Arg	Ser 455	Ser	Thr	Ser	Thr	Trp 460	Gly	Tyr	Phe	Ser
Val 465	-	Thr	Ser	Gly	Ala 470	Leu	His	Glu	Tyr	Ala 475	Asp	Ser	Gln	Phe	Gly 480
				_	Gly			_				_	_		Met
Val	Ile	Ser	Leu 500	Lys	Glu	Leu	Ser	Ile 505	Arg	Gly	Asp	Phe	Arg 510	Thr	Thr
Val	Glu	Tyr 515	Leu	Ile	Lys	Leu	Leu 520	Glu	Thr	Asp	Ala	Phe 525	Glu	Ser	Asn
Lys	Ile 530	Thr	Thr	Gly	Trp	Leu 535	Asp	Gly	Leu	Ile	Gln 540	Asp	Arg	Leu	Thr

<210> <211> <212> PRT Ustilago maydis <213> <220> MISC_FEATURE <221> <222> (1)..(539)N- and C-terminal deleted Ustilago ACCase BC domain (AAs 12-550) <400> 29 Phe Ile Gly Gly Asn Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly

Ala Glu Arg Pro Pro

Ile	Lys	Glu	Thr 180	Met	Met	Ser	Asp	Gln 185	Gly	Phe	Leu	Thr	Val 190	Ser	Asp
Asp	Val	Tyr 195	Gln	Gln	Ala	Cys	Ile 200	His	Thr	Ala	Glu	Glu 205	Gly	Leu	Glu
Lys	Ala 210	Glu	Lys	Ile	Gly	Tyr 215	Pro	Val	Met	Ile	Lys 220	Ala	Ser	Glu	Gly
Gly 225	Gly	Gly	Lys	Gly	Ile 230	Arg	Lys	Cys	Thr	Asn 235	Gly	Glu	Glu	Phe	Lys 240
Gln	Leu	Tyr	Asn	Ala 245	Val	Leu	Gly	Glu	Val 250	Pro	Gly	Ser	Pro	Val 255	Phe
Val	Met	Lys	Leu 260	Ala	Gly	Gln	Ala	Arg 265	His	Leu	Glu	Val	Gln 270	Leu	Leu
Ala	Asp	Gln 275	-	Gly	Asn	Ala	Ile 280	Ser	Ile	Phe	Gly	Arg 285	Asp	Cys	Ser
Val	Gln 290	Arg	Arg	His	Gln	Lys 295	Ile	Ile	Glu	Glu	Ala 300	Pro	Val	Thr	Ile
Ala 305		Glu	Asp	Ala	Arg 310	Glu	Ser	Met	Glu	Lys 315	Ala	Ala	Val	Arg	Leu 320
Ala	Lys	Leu	Val	Gly 325		Val	Ser	Ala	Gly 330	Thr	Val	Glu	Trp	Leu 335	Tyr
Ser	Pro	Glu	Ser 340	Gly	Glu	Phe	Ala	Phe 345	Leu	Glu	Leu	Asn	Pro 350	Arg	Leu
Gln	Val										Gly			Ile	Pro
Ala	Ala 370	Gln	Leu	Gln	Val	Ala 375	Met	Gly	Ile	Pro	Leu 380	Tyr	Ser	Ile	Arg
Asp 385		Arg	Thr	Leu	Tyr 390	Gly	Met	Asp	Pro	Arg 395	Gly	Asn	Glu	Val	Ile 400
Asp	Phe	Asp	Phe	Ser 405	Ser	Pro	Glu	Ser	Phe 410	Lys	Thr	Gln	Arg	Lys 415	Pro
Gln	Pro	Gln	Gly	His	Val	Val	Ala	Cys	Arg	Ile	Thr	Ala	Glu	Asn	Pro

420 425 430

Asp Thr Gly Phe Lys Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe 435 440 445

Arg Ser Ser Thr Ser Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly 450 460

Ala Leu His Glu Tyr Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr 465 470 475 480

Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys 485 490 495

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 500 505 510

Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly 515 520 525

Trp Leu Asp Gly Leu Ile Gln Asp Arg Leu Thr 530 535

<210> 30

<211> 529

<212> PRT

<213> Ustilago maydis

<220>

<221> MISC FEATURE

<222> (1)..(529)

<223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 17-545)

<400> 30

Pro Leu Glu Thr Ala Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys
1 5 10 15

Gln Gly Gly His Ser Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly 20 25 30

Ile Ala Val Lys Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu
35 40 45

Thr Phe Gly Asp Glu Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro 50 55 60

Glu Asp Leu Lys Val Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr

Val Glu Val Pro Gly Gly Ser Asn Asn Asn Asn Tyr Ala Asn Val Asp 85 90 95

Leu Ile Val Asp Val Ala Glu Arg Ala Gly Val His Ala Val Trp Ala 100 105 110

Gly Trp Gly His Ala Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala 115 120 125

Ala Ser Lys His Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met 130 135 140

Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala 145 150 150

Asp Val Pro Cys Met Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met 165 170 175

Met Ser Asp Gln Gly Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln 180 185 190

Ala Cys Ile His Thr Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile 195 200 205

Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly 210 215 220

Ile Arg Lys Cys Thr Asn Gly Glu Glu Phe Lys Gln Leu Tyr Asn Ala 225 230 235 240

Val Leu Gly Glu Val Pro Gly Ser Pro Val Phe Val Met Lys Leu Ala 245 250 255

Gly Gln Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly 260 265 270

Asn Ala Ile Ser Ile Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His 275 280 285

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Pro Glu Asp Ala 290 295 300

Arg Glu Ser Met Glu Lys Ala Ala Val Arg Leu Ala Lys Leu Val Gly 305 310 315 320

Tyr Val Ser Ala Gly Thr Val Glu Trp Leu Tyr Ser Pro Glu Ser Gly 325 330 335

Glu Phe Ala Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro 340 345 350

Thr Thr Glu Met Val Ser Gly Val Asn Ile Pro Ala Ala Gln Leu Gln 355 360 365

Val Ala Met Gly Ile Pro Leu Tyr Ser Ile Arg Asp Ile Arg Thr Leu 370 380

Tyr Gly Met Asp Pro Arg Gly Asn Glu Val Ile Asp Phe Asp Phe Ser 385 390 395 400

Ser Pro Glu Ser Phe Lys Thr Gln Arg Lys Pro Gln Pro Gln Gly His
405 410 415

Val Val Ala Cys Arg Ile Thr Ala Glu Asn Pro Asp Thr Gly Phe Lys
420 425 430

Pro Gly Met Gly Ala Leu Thr Glu Leu Asn Phe Arg Ser Ser Thr Ser 435 440 445

Thr Trp Gly Tyr Phe Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr 450 455 460

Ala Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser 465 470 475 480

Glu Ala Arg Lys Gln Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg 485 490 495

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr 500 510

Asp Ala Phe Glu Ser Asn Lys Ile Thr Thr Gly Trp Leu Asp Gly Leu 515 520 525

Ile

<210> 31

<211> 519

<212> PRT

- <213> Ustilago maydis
- <220>
- <221> MISC_FEATURE
- <222> (1)..(519)
- <223> N- and C-terminal deleted Ustilago ACCase BC domain (AAs 22-540)
- <400> 31
- Pro Ala Ser Pro Val Ala Asp Phe Ile Arg Lys Gln Gly Gly His Ser 1 10 15
- Val Ile Thr Lys Val Leu Ile Cys Asn Asn Gly Ile Ala Ala Val Lys 20 25 30
- Glu Ile Arg Ser Ile Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu
 35 40 45
- Arg Ala Ile Glu Phe Thr Val Met Ala Thr Pro Glu Asp Leu Lys Val 50 60
- Asn Ala Asp Tyr Ile Arg Met Ala Asp Gln Tyr Val Glu Val Pro Gly 65 70 75 80
- Gly Ser Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Val
 85 90 95
- Ala Glu Arg Ala Gly Val His Ala Val Trp Ala Gly Trp Gly His Ala
 100 105 110
- Ser Glu Asn Pro Arg Leu Pro Glu Ser Leu Ala Ala Ser Lys His Lys 115 120 125
- Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp 130 135 140
- Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Asp Val Pro Cys Met 145 150 155 160
- Pro Trp Ser Gly Thr Gly Ile Lys Glu Thr Met Met Ser Asp Gln Gly 165 170 175
- Phe Leu Thr Val Ser Asp Asp Val Tyr Gln Gln Ala Cys Ile His Thr 180 185 190
- Ala Glu Glu Gly Leu Glu Lys Ala Glu Lys Ile Gly Tyr Pro Val Met 195 200 205

Ile	Lys 210	Ala	Ser	Glu	Gly	Gly 215	Gly	Gly	Lys	Gly	Ile 220	Arg	Lys	Cys	Thr
Asn 225	Gly	Glu	Glu	Phe	Lys 230	Gln	Leu	Tyr	Asn	Ala 235	Val	Leu	Gly	Glu	Val 240
Pro	Gly	Ser	Pro	Val 245	Phe	Val	Met	Lys	Leu 250	Ala	Gly	Gln	Ala	Arg 255	His
Leu	Glu	Val	Gln 260	Leu	Leu	Ala	Asp	Gln 265	Tyr	Gly	Asn	Ala	Ile 270	Ser	Ile
Phe	Gly	Arg 275	Asp	Cys	Ser	Val	Gln 280	Arg	Arg	His	Gln	Lys 285	Ile	Ile	Glu
Glu	Ala 290	Pro	Val	Thr	Ile	Ala 295	Pro	Glu	Asp	Ala	Arg 300	Glu	Ser	Met	Glu
Lys 305	Ala	Ala	Val	Arg	Leu 310	Ala	Lys	Leu	Val	Gly 315		Val	Ser	Ala	Gly 320
Thr	Val	Glu	Trp	Leu 325		Ser	Pro	Glu	Ser 330	Gly	Glu	Phe	Ala	Phe 335	Leu
Glu	Leu	Asn	Pro 340	Arg	Leu	Gln	Val	Glu 345	His	Pro	Thr	Thr	Glu 350	Met	Val
Ser	Gly	Val 355		Ile	Pro	Ala	Ala 360	Gln	Leu	Gln	Val	Ala 365	Met	Gly	Ile
Pro	Leu 370	Tyr	Ser	Ile	Arg	Asp 375		Arg	Thr	Leu	Tyr 380	Gly	Met	Asp	Pro
Arg 385	Gly	Asn					Phe								Phe 400
Lys	Thr	Gln	Arg	Lys 405	Pro	Gln	Pro	Gln	Gly 410	His	Val	Val	Ala	Cys 415	Arg
Ile	Thr	Ala	Glu 420	Asn	Pro	Asp	Thr	Gly 425	Phe	Lys	Pro	Gly	Met 430	Gly	Ala
Leu	Thr	Glu 435		Asn	Phe	Arg	Ser 440	Ser	Thr	Ser	Thr	Trp 445	Gly	Tyr	Phe

Ser Val Gly Thr Ser Gly Ala Leu His Glu Tyr Ala Asp Ser Gln Phe 450 455 460

Gly His Ile Phe Ala Tyr Gly Ala Asp Arg Ser Glu Ala Arg Lys Gln 465 470 475 480

Met Val Ile Ser Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr 485 490 495

Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Asp Ala Phe Glu Ser 500 510

Asn Lys Ile Thr Thr Gly Trp
515

- <210> 32
- <211> 580
- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC FEATURE
- <222> (76)..(76)
- <223> Saccharomyces cerevisiae ACCase BC domain S77Y mutation
- <400> 32

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Tyr Val Arg Lys Trp 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110

Asp	Gln	Tyr 115	Ile	Glu	Val	Pro	Gly 120	Gly	Thr	Asn	Asn	Asn 125	Asn	Tyr	Ala
Asn	Val 130	Asp	Leu	Ile	Val	Asp 135	Ile	Ala	Glu	Arg	Ala 140	Asp	Val	Asp	Ala
Val 145	Trp	Ala	Gly	Trp	Gly 150	His	Ala	Ser	Glu	Asn 155	Pro	Leu	Leu	Pro	Glu 160
Lys	Leu	Ser	Gln	Ser 165	Lys	Arg	Lys	Val	Ile 170	Phe	Ile	Gly	Pro	Pro 175	Gly
Asn	Ala	Met	Arg 180	Ser	Leu	Gly	Asp	Lys 185	Ile	Ser	Ser	Thr	Ile 190	Val	Ala
Gln	Ser	Ala 195	Lys	Val	Pro	Cys	Ile 200	Pro	Trp	Ser	Gly	Thr 205	Gly	Val	Asp
Thr	Val 210	His	Val	Asp	Glu	Lys 215	Thr	Gly	Leu	Val	Ser 220	Val	Asp	Asp	Asp
Ile 225	_	Gln	Lys	Gly	Cys 230	Cys	Thr	Ser	Pro	Glu 235	Asp	Gly	Leu	Gln	Lys 240
Ala	Lys	Arg	Ile	Gly 245		Pro	Val	Met	Ile 250		Ala	Ser	Glu	Gly 255	Gly
Gly	Gly	Lys	Gly 260	Ile	Arg	Gln	Val	Glu 265	Arg	Glu	Glu	Asp	Phe 270	Ile	Ala
Leu	Tyr	His 275		Ala	Ala	Asn	Glu 280		Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met					Arg								Leu	Leu	Ala
Asp 305		Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315	Arg	Asp	Cys	Ser	Val 320
Gln	Arg	Arg	His	Gln 325		Ile	Ile	Glu	Glu 330		Pro	Val	Thr	Ile 335	Ala
Lys	Ala	Glu	Thr 340		His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Lys	Leu	Val	Gly	Tyr	Val	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Leu	Tyr	Ser

355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln 370 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 560

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro 565 570 575

Thr Leu Ala Val 580

<210> 33 <211> 575

- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC FEATURE
- <222> (1)..(575)
- <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
 7-581)
- <400> 33
- Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser 1 10 15
- Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val 20 25 30
- Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly 35 40 45
- Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala 50 60
- Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe 70 75 80
- Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp 90 95
- Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu 100 105 110
- Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile 115 120 125
- Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp 130 135 140
- Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser 145 150 155 160
- Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser 165 170 175
- Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
 180 185 190
- Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp

195 200 205

Gl	u Lys 210		Gly	Leu	Val	Ser 215	Val	Asp	Asp	Asp	Ile 220	Tyr	Gln	Lys	Gly
Су 22	s Cys 5	Thr	Ser	Pro	Glu 230	Asp	Gly	Leu	Gln	Lys 235	Ala	Lys	Arg	Ile	Gly 240
Ph	e Pro	Val	Met	Ile 245	Lys	Ala	Ser	Glu	Gly 250	_	Gly	Gly	Lys	Gly 255	Ile
Ar	g Gln	Val	Glu 260	Arg	Glu	Glu	Asp	Phe 265	Ile	Ala	Leu	Tyr	His 270	Gln	Ala
Al	a Asn	Glu 275	Ile	Pro	Gly	Ser	Pro 280	Ile	Phe	Ile	Met	Lys 285	Leu	Ala	Gly
Ar	g Ala 290	_	His				Gln						Tyr	Gly	Thr
As:	n Ile 5	Ser	Leu	Phe	Gly 310	Arg	Asp	Cys	Ser	Val 315	Gln	Arg	Arg	His	Gln 320
Ly	s Ile	Ile	Glu	Glu 325	Ala	Pro	Val	Thr	Ile 330	Ala	Lys	Ala	Glu	Thr 335	Phe
Hi	s Glu	Met	Glu 340	Lys	Ala	Ala	Val	Arg 345	Leu	Gly	Lys	Leu	Val 350	Gly	Tyr
Va	l Ser	Ala 355	Gly	Thr	Val	Glu	Tyr 360	Leu	Tyr	Ser	His	Asp 365	Asp	Gly	Lys
Ph	e Tyr 370	Phe	Leu	Glu	Leu	Asn 375	Pro	Arg	Leu	Gln	Val 380	Glu	His	Pro	Thr
Th:	r Glu 5	Met	Val	Ser	Gly 390	Val	Asn	Leu	Pro	Ala 395	Ala	Gln	Leu	Gln	Ile 400
Ala	a Met	Gly	Ile	Pro 405	Met	His	Arg	Ile	Ser 410	Asp	Ile	Arg	Thr	Leu 415	Tyr
Gl	y Met	Asn	Pro 420	His	Ser	Ala	Ser	Glu 425	Ile	Asp	Phe	Glu	Phe 430	Lys	Thr
Gl	n Asp	Ala	Thr	Lys	Lys	Gln	Arg	Arg	Pro	Ile	Pro	Lys	Gly	His	Cys

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro 450 460

Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
465 470 475 480

Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser 485 490 495

Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala 500 505 510

Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly 515 520 525

Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu 530 540

Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile 545 550 550

Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 565 570 575

<210> 34

<211> 570

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(570)

<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs
12-581)

<400> 34

Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu
1 10 15

Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu 20 25 30

Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile 35 40 45

Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile

50 55 60

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu

Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe

Gly 305		Asp	Cys	Ser	Val 310		Arg	Arg	His	Gln 315		Ile	Ile	Glu	Glu 320
Ala	Pro	Val	Thr	Ile 325	Ala	Lys	Ala	Glu	Thr 330		His	Glu	Met	Glu 335	Lys
Ala	Ala	Val	Arg 340		Gly	Lys	Leu	Val 345		Tyr	Val	Ser	Ala 350	Gly	Thr
Val	Glu	Tyr 355	Leu	Tyr	Ser	His		Asp		Lys	Phe	Tyr 365	Phe	Leu	Glu
Leu	Asn 370	Pro	Arg	Leu	Gln	Val 375	Glu	His	Pro	Thr	Thr 380	Glu	Met	Val	Ser
Gly 385	Val	Asn	Leu	Pro	Ala 390	Ala	Gln	Leu	Gln	Ile 395	Ala	Met	Gly	Ile	Pro 400
Met	His	Arg	Ile	Ser 405	Asp	Ile	Arg	Thr	Leu 410	Tyr	Gly	Met	Asn	Pro 415	His
Ser	Ala	Ser	Glu 420	Ile	Asp	Phe	Glu	Phe 425	Lys	Thr	Gln	Asp	Ala 430	Thr	Lys
Lys	Gln	Arg 435	Arg	Pro	Ile	Pro	Lys 440	Gly	His	Cys	Thr	Ala 445	Cys	Arg	Ile
Thr	Ser 450	Glu	Asp	Pro	Asn	Asp 455	Gly	Phe	Lys	Pro	Ser 460	Gly	Gly	Thr	Leu
His 465	Glu	Leu	Asn	Phe	Arg 470	Ser	Ser	Ser	Asn	Val 475	Trp	Gly	Tyr	Phe	Ser 480
Val									Phe 490		-				Gly
His	Ile	Phe	Ala 500	Phe	Gly	Glu	Asn	Arg 505	Gln	Ala	Ser	Arg	Lys 510	His	Met
Val	Val	Ala 515	Leu	Lys	Glu	Leu	Ser 520	Ile	Arg	Gly	Asp	Phe 525	Arg	Thr	Thr
Val	Glu 530	Tyr	Leu	Ile	Lys	Leu 535	Leu	Glu	Thr	Glu	Asp 540	Phe	Glu	Asp	Asn

Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr 545 550 560

Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 565 570

- <210> 35
- <211> 560
- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC_FEATURE
- <222> (1)..(560)
- <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 22-581)
- <400> 35
- Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr 1 5 10
- Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His 20 25 30
- Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile 35 40 45
- Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr 50 60
- Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu
 65 70 75 80
- Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile 85 90 95
- Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu 100 105 110
- Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly
 115 120 125
- Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln 130 135 140
- Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg 145 150 155 160

Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	Ser	Ala 175	Lys
Val	Pro	Cys	Ile 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Val	Asp	Thr	Val 190	His	Val
Asp	Glu	Lys 195	Thr	Gly	Leu	Val	Ser 200	Val	Asp	Asp	Asp	Ile 205	Tyr	Gln	Lys
Gly	Cys 210	Cys	Thr	Ser	Pro	Glu 215	Asp	Gly	Leu	Gln	Lys 220	Ala	Lys	Arg	Ile
Gly 225	Phe	Pro	Val	Met	Ile 230	Lys	Ala	Ser	Glu	Gly 235	Gly	Gly	Gly	Lys	Gly 240
Ile	Arg	Gln	Val	Glu 245	Arg	Glu	Glu	Asp	Phe 250	Ile	Ala	Leu	Tyr	His 255	Gln
Ala	Ala	Asn	Glu 260	Ile	Pro	Gly	Ser	Pro 265	Ile	Phe	·Ile	Met	Lys 270	Leu	Ala
Gly	Arg	Ala 275	Arg	His	Leu	Glu	Val 280	Gln	Leu	Leu	Ala	Asp 285	Gln	Tyr	Gly
Thr	Asn 290	Ile	Ser	Leu	Phe	Gly 295	Arg	Asp	Cys	Ser-	Val 300	Gln	Arg	Arg	His
Gln 305	Lys	Ile	Ile	Glu	Glu 310	Ala	Pro	Val	Thr	Ile 315	Ala	Lys	Ala	Glu	Thr 320
Phe	His	Glu	Met	Glu 325	Lys	Ala	Ala	Val	Arg 330	Leu	Gly	Lys	Leu	Val 335	Gly
Tyr	Val	Ser	Ala 340	Gly	Thr	Val	Glu	Tyr 345	Leu	Tyr	Ser	His	Asp 350	Asp	Gly
Lys	Phe	Tyr 355	Phe	Leu	Glu	Leu	Asn 360	Pro	Arg	Leu	Gln	Val 365	Glu	His	Pro
Thr	Thr 370	Glu	Met	Val	Ser	Gly 375	Val	Asn	Leu	Pro	Ala 380	Ala	Gln	Leu	Gln
Ile 385	Ala	Met	Gly	Ile	Pro 390	Met	His	Arg	Ile	Ser 395	Asp	Ile	Arg	Thr	Leu 400

Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys 405 410 415

Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His 420 425 430

Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys
435
440
445

Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn 450 455 460

Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe 465 470 475 480

Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln 485 490 495

Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg 500 510

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr 515 520 525

Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu 530 540

Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 545 550 550 560

<210> 36

<211> 550

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(550)

<223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 32-581

<400> 36

Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg
1 10 15

Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu 20 25 30

Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp 185 190 Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile

Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg

Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu

Leu	Ala	Asp 275	Gln	Tyr	Gly	Thr	Asn 280	Ile	Ser	Leu	Phe	Gly 285	Arg	Asp	Cys
Ser	Val 290	Gln	Arg	Arg	His	Gln 295	Lys	Ile	Ile	Glu	Glu 300	Ala	Pro	Val	Thr
Ile 305	Ala	Lys	Ala	Glu	Thr 310	Phe	His	Glu	Met	Glu 315	Lys	Ala	Ala	Val	Arg 320
Leu	Gly	Lys	Leu	Val 325	Gly	Tyr	Val	Ser	Ala 330	Gly	Thr	Val	Glu	Tyr 335	Leu
Tyr	Ser	His	Asp 340	Asp	Gly	Lys	Phe	Tyr 345	Phe	Leu	Glu	Leu	Asn 350	Pro	Arg
Leu	Gln	Val 355	Glu	His	Pro	Thr	Thr 360	Glu	Met	Val	Ser	Gly 365	Val	Asn	Leu
Pro	Ala 370	Ala	Gln	Leu	Gln	Ile 375	Ala	Met	Gly	Ile	Pro 380	Met	His	Arg	Ile
Ser 385	_	Ile	Arg	Thr	Leu 390	Tyr	Gly	Met	Asn	Pro 395	His	Ser	Ala	Ser	Glu 400
Ile	Asp	Phe	Glu	Phe 405	Lys	Thr	Gln	Asp	Ala 410	Thr	Lys	Lys	Gln	Arg 415	Arg
Pro	Ile	Pro	Lys 420	Gly	His	Cys	Thr	Ala 425	Cys	Arg	Ile	Thr	Ser 430	Glu	Asp
Pro	Asn	Asp 435	Gly	Phe	Lys	Pro	Ser 440	Gly	Gly	Thr	Leu	His 445	Glu	Leu	Asn
Phe	Arg 450	Ser	Ser	Ser		Val 455	_	_	Tyr		Ser 460		Gly	Asn	Asn
Gly 465	Asn	Ile	His	Ser	Phe 470	Ser	Asp	Ser	Gln	Phe 475	Gly	His	Ile	Phe	Ala 480
Phe	Gly	Glu	Asn	Arg 485	Gln	Ala	Ser	Arg	Lys 490	His	Met	Val	Val	Ala 495	Leu
Lys	Glu	Leu	Ser 500	Ile	Arg	Gly	Asp	Phe 505	Arg	Thr	Thr	Val	Glu 510	Tyr	Leu

- Ile Lys Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr 515 520 525
- Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro 530 540

Asp Pro Thr Leu Ala Val 545 550

- <210> 37
- <211> 540
- <212> PRT
- <213> Saccharomyces cerevisiae

<220>

- <221> MISC_FEATURE
- <222> (1)..(540)
- <223> N-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 42-581)

<400> 37

- Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr 1 5 10
- Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 20 25 30
- Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Asp 35 40 45
- Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu Ala 50 55 60
- Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro Gly 65 70 75 80
- Gly Thr Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile 85 90 95
- Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110
- Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys
 115 120 125
- Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp 130 135 140

Lys 145	Ile	Ser	Ser	Thr	Ile 150	Val	Ala	Gln	Ser	Ala 155	Lys	Val	Pro	Cys	Ile 160
Pro	Trp	Ser	Gly	Thr 165	Gly	Val	Asp	Thr	Val 170	His	Val	Asp	Glu	Lys 175	Thr
Gly	Leu	Val	Ser 180	Val	Asp	Asp	Asp	Ile 185	Tyr	Gln	Lys	Gly	Cys 190	Cys	Thr
Ser	Pro	Glu 195	Asp	Gly	Leu	Gln	Lys 200	Ala	Lys	Arg	Ile	Gly 205	Phe	Pro	Val
Met	Ile 210	Lys	Ala	Ser	Glu	Gly 215	Gly	Gly	Gly	Lys	Gly 220	Ile	Arg	Gln	Val
Glu 225	Arg	Glu	Glu	Asp	Phe 230	Ile	Ala	Leu	Tyr	His 235	Gln	Ala	Ala	Asn	Glu 240
Ile	Pro	Gly	Ser	Pro 245	Ile	Phe	Ile	Met	Lys 250		Ala	Gly	Arg	Ala 255	Arg
His	Leu	Glu	Val 260	Gln	Leu	Leu	Ala	Asp 265	Gln	Tyr	Gly	Thr	Asn 270	Ile	Ser
Leu	Phe	Gly 275	-	Asp	Cys	Ser	Val 280	Gln	Arg	Arg	His	Gln 285	Lys	Ile	Ile
Glu	Glu 290	Ala	Pro	Val	Thr	Ile 295	Ala	Lys	Ala	Glu	Thr 300	Phe	His	Glu	Met
Glu 305		Ala	Ala	Val	Arg 310	Leu	Gly	Lys	Leu	Val 315	Gly	Tyr	Val	Ser	Ala 320
Gly	Thr	Val	Glu						Asp 330					Tyr 335	Phe
Leu	Glu	Leu	Asn 340	Pro	Arg	Leu	Gln	Val 345	Glu	His	Pro	Thr	Thr 350	Glu	Met
Val	Ser	Gly 355	Val	Asn	Leu	Pro	Ala 360	Ala	Gln	Leu	Gln	Ile 365	Ala	Met	Gly
Ile	Pro 370	Met	His	Arg	Ile	Ser 375	Asp	Ile	Arg	Thr	Leu 380	Tyr	Gly	Met	Asn

Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val <210> 38 <211> 575 <212> PRT <213> Saccharomyces cerevisiae <220> <221> MISC FEATURE <222> (1)..(575) <223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-576) <400> 38 Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile

Gly Leu As		Asp Lys	Leu Gl 40	u Glu	Ser Pro	Leu Ar 45	g Asp	Phe
Val Lys Se 50	er His Gly	Gly His 55	Thr Va	al Ile	Ser Lys 60	Ile Le	eu Ile	Ala
Asn Asn Gi 65	ly Ile Ala	Ala Val 70	Lys Gl		Arg Ser 75	Val Ar	g Lys	Trp 80
Ala Tyr G	lu Thr Phe 85	Gly Asp	Asp Ar	g Thr 90	Val Gln	Phe Va	al Ala 95	Met
Ala Thr P	ro Glu Asp 100	Leu Glu	Ala As		Glu Tyr	Ile Ar	_	Ala
-	yr Ile Glu 15	Val Pro	Gly Gl 120	ly Thr	Asn Asn	Asn As	sn Tyr	Ala
Asn Val As	sp Leu Ile	Val Asp 135		la Glu	Arg Ala 140	Asp Va	al Asp	Ala
Val Trp A	la Gly Trp	Gly His 150	Ala Se		Asn Pro 155	Leu Le	eu Pro	Glu 160
Lys Leu S	er Gln Ser 165		Lys Va	al Ile 170	Phe Ile	Gly Pr	ro Pro 175	Gly
Asn Ala M	et Arg Ser 180	Leu Gly	Asp Ly 18		Ser Ser	Thr II		Ala
	la Lys Val 95	Pro Cys	Ile Pr 200	o Trp	Ser Gly	Thr Gl 205	ly Val	Asp
Thr Val H	is Val Asp	Glu Lys 215	Thr Gl	y Leu	Val Ser 220	Val As	sp Asp	Asp
Ile Tyr G	ln Lys Gly	Cys Cys 230	Thr Se		Glu Asp 235	Gly Le	eu Gln	Lys 240
Ala Lys A	rg Ile Gly 245		Val Me	et Ile 250	Lys Ala	Ser Gl	u Gly 255	Gly
Gly Gly L	ys Gly Ile 260	Arg Gln	Val Gl 26	_	Glu Glu	Asp Ph		Ala

Leu Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile
Met Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala
Asp Gln 305	Tyr	Gly	Thr	Asn 310	Ile	Ser	Leu	Phe	Gly 315	Arg	Asp	Cys	Ser	Val 320
Gln Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala
Lys Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly
Lys Leu	Val 355	Gly	Tyr	Vаl	Ser	Ala 360	Gly	Thr	Val	Glu	Tyr 365	Leu	Tyr	Ser
His Asp 370	Asp	Gly	Lys	Phe	Tyr 375	Phe	Leu	Glu	Leu	Asn 380	Pro	Arg	Leu	Gln
Val Glu 385	His	Pro	Thr	Thr 390	Glu	Met	Val	Ser	Gly 395	Val	Asn	Leu	Pro	Ala 400
Ala Gln	Leu	Gln	Ile 405	_	Met	Gly	Ile	Pro 410	Met	His	Arg	Ile	Ser 415	Asp
Ile Arg	Thr	Leu 420	Tyr	Gly	Met	Asn	Pro 425	His	Ser	Ala	Ser	Glu 430	Ile	Asp
Phe Glu	Phe 435	Lys	Thr	Gln	Asp	Ala 440	Thr	Lys	Lys	Gln	Arg 445	Arg	Pro	Ile
Pro Lys 450	Gly	His	Cys	Thr	Ala 455	Cys	Arg	Ile	Thr	Ser 460	Glu	Asp	Pro	Asn
Asp Gly 465	Phe	Lys	Pro	Ser 470	Gly	Gly	Thr	Leu	His 475	Glu	Leu	Asn	Phe	Arg 480
Ser Ser	Ser	Asn	Val 485	Trp	Gly	Tyr	Phe	Ser 490	Val	Gly	Asn	Asn	Gly 495	Asn
Ile His	Ser	Phe 500	Ser	Asp	Ser	Gln	Phe 505	Gly	His	Ile	Phe	Ala 510	Phe	Gly
Glu Asn	Arg	Gln	Ala	Ser	Arg	Lys	His	Met	Val	Val	Ala	Leu	Lys	Glu

515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 550

Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp 565 570 575

<210> 39

<211> 570

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC_FEATURE

<222> (1)..(570)

<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-571)

<400> 39

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp

70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125

Asn	Val 130	Asp	Leu	Ile	Val	Asp 135	Ile	Ala	Glu	Arg	Ala 140	Asp	Val	Asp	Ala	
Val 145	Trp	Ala	Gly	Trp	Gly 150	His	Ala	Ser	Glu	Asn 155	Pro	Leu	Leu	Pro	Glu 160	
Lys	Leu	Ser	Gln	Ser 165	Lys	Arg	Lys	Val	Ile 170	Phe	Ile	Gly	Pro	Pro 175	Gly	
Asn	Ala	Met	Arg 180	Ser	Leu	Gly	Asp	Lys 185	Ile	Ser	Ser	Thr	Ile 190	Val	Ala	
Gln	Ser	Ala 195	Lys	Val	Pro	Cys	Ile 200	Pro	Trp	Ser	Gly	Thr 205	Gly	Val	Asp	
Thr	Val 210	His	Val	Asp	Glu	Lys 215	Thr	Gly	Leu	Val	Ser 220	Val	Asp	Asp	Asp	
Ile 225	Tyr	Gln	Lys	Gly	Cys 230	Cys	Thr	Ser	Pro	Glu 235	Asp	Gly	Leu	Gln	Lys 240	
Ala	Lys	Arg	Ile	Gly 245	Phe	Pro	Val	Met	Ile 250	Lys	Ala	Ser	Glu	Gly 255	Gly	
Gly	Gly	Lys	Gly 260	Ile	Arg	Gln	Val	Glu 265	Arg	Glu	Glu	Asp	Phe 270	Ile	Ala	
Leu	Tyr	His 275	Gln	Ala	Ala	Asn	Glu 280	Ile	Pro	Gly	Ser	Pro 285	Ile	Phe	Ile	
Met	Lys 290	Leu	Ala	Gly	Arg	Ala 295	Arg	His	Leu	Glu	Val 300	Gln	Leu	Leu	Ala	
Asp 305			Gly		Asn 310			Leu			Arg				Val 320	
Gln	Arg	Arg	His	Gln 325	Lys	Ile	Ile	Glu	Glu 330	Ala	Pro	Val	Thr	Ile 335	Ala	
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345	Lys	Ala	Ala	Val	Arg 350	Leu	Gly	
Lys	Leu	Val 355	Gly	Tyr	Val	Ser	Ala 360	Gly	Thr	Val	Glu	Tyr 365	Leu	Tyr	Ser	
His	Asp	Asp	Gly	Lys	Phe	Tyr	Phe	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	

370 375 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp
420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp
545 550 555 560

Leu Asp Asp Leu Ile Thr His Lys Met Thr 565 570

<210> 40

<211> 560

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC_FEATURE

<222> (1)..(560)

<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs

2-561)

<400> 40

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1 10 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile
20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp

70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 210 220

Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys

Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly 245 250 255

Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala 260 265 270

Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile 275 280 285

Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala 290 295 300

Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val 305 310 315 320

Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala 325 330 335

Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln 370 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 540

Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp 545 550 550

<210> 41

<211> 550

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(550)

<223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-551)

<400> 41

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu
1 1 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe
35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55 60

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met 85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala

- Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125
- Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140
- Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160
- Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 165 170 175
- Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190
- Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205
- Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Asp 210 215 220
- Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys 235 230 235
- Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly 245 250 255
- Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala 260 265 270
- Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile 275 280 285
- Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala 290 295 300
- Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val 305 310 315 320
- Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala 325 330 335
- Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly 340 345 350

Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser 355 360 365

His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln 370 380

Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala 385 390 395 400

Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp 405 410 415

Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp 420 425 430

Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile 435 440 445

Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn 450 455 460

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg 465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu 515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys 530 540

Leu Leu Glu Thr Glu Asp 545 550

<210> 42

<211> 540

<212> PRT

<213> Saccharomyces cerevisiae

<220>

- <221> MISC_FEATURE
- <222> (1)..(540)
- <223> C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 2-541)

<400> 42

Ser Glu Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu 1 5 15

Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile 20 25 30

Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe 35 40 45

Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala 50 55

Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp 65 70 75 80

Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met
85 90 95

Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala 100 105 110

Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala 115 120 125

Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala 130 135 140

Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu 145 150 155 160

Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly 165 170 175

Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala 180 185 190

Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp 195 200 205

Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp 210 215 220

225	e Ty:	r GI:	n Ly:	s Gly	y Cys 230	s Cy:	s Th	r Se	r Pr	0 Gl: 23		p Gl	y Lei	u Gl	n Lys 240
Ala	a Lys	s Ar	g Ile	e Gly 245	y Phe	e Pro	o Val	l Met	250		s Ala	a Se:	r Glı	u Gl ₃ 25!	y Gly 5
Gly	/ Gly	y Ly:	s Gl ₃ 260	/ Il∈	e Arg	g Glr	n Val	l Gli 265		g Glı	ı Glı	ı Ası	o Phe 270		∋ Ala
Leu	а Туз	C His	s Glr	n Ala	a Ala	ı Asr	1 Glu 280	ı Ile	e Pro	o Gly	y Sei	285		e Phe	e Ile
Met	Lys 290	s Lei	ı Ala	Gly	/ Arg	Ala 295		, His	. Leu	ı Glı	1 Val 300		ı Lev	ı Lev	ı Ala
Asp 305	Gln	туг	Gly	Thr	Asn 310	Ile	e Ser	Leu	. Phe	Gly 315		J Asp	Cys	s Ser	Val 320
Gln	Arg	Arg	, His	Gln 325	Lys	Ile	: Ile	Glu	Glu 330		Pro	Val	. Thr	335	Ala
Lys	Ala	Glu	Thr 340	Phe	His	Glu	Met	Glu 345		Ala	. Ala	Val	Arg 350		Gly
Lys	Leu	Val 355	Gly	Tyr	Val	Ser	Ala 360		Thr	Val	Glu	Tyr 365		Tyr	Ser
His	Asp 370	Asp	Gly	Lys	Phe	Tyr 375	Phe	Leu	Glu	Leu	Asn 380	Pro	Arg	Leu	Gln
Val 385	Glu	His	Pro	Thr	Thr 390	Glu	Met	Val	Ser	Gly 395	Val	Asn	Leu	Pro	Ala 400
Ala	Gln	Leu	Gln	Ile 405	Ala	Met	Gly	Ile	Pro 410	Met	His	Arg	Ile	Ser 415	Asp
Ile	Arg	Thr	Leu 420	Tyr	Gly	Met	Asn	Pro 425	His	Ser	Ala	Ser	Glu 430	Ile	Asp
Phe	Glu	Phe 435	Lys	Thr	Gln	Asp	Ala 440	Thr	Lys	Lys	Gln	Arg 445	Arg	Pro	Ile
Pro	Lys 450	Gly	His	Cys	Thr	Ala 455	Cys	Arg	Ile	Thr	Ser 460	Glu	Asp	Pro	Asn

Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg
465 470 475 480

Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn 485 490 495

Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly 500 505 510

Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu
515 520 525

Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu 530 535 540

<210> 43

<211> 575

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC_FEATURE

<222> (1)..(575)

<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
domain (AAs 4-578)

<400> 43

Glu Ser Leu Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr 5 10 15

Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu 20 25 30

Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys 35 40 45

Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn 50 55 60

Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr
65 75 80

Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr 85 90 95

Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln 100 105 110

Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys Thr Gly Leu Val Ser Val Asp Asp Ile Tyr Gln Lys Gly Cys Cys Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Gln Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu

Val	Gly	Tyr 355	Val	Ser	Ala	_	Thr 360	Val	Glu	Tyr	Leu	Tyr 365	Ser	His	Asp

Asp Gly Lys	Phe Tyr	Phe 1	Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	Val	Glu
370		:	375					380				

His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln 385 390 395 400

Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg
405 410 415

Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu 420 425 430

Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys 435 440 445

Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly 450 455 460

Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser 465 470 475 480

Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His 485 490 495

Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn 500 505 510

Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser 515 520 525

Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu 530 540

Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp 545 550 550

Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp Pro Thr 565 570 575

<210> 44

<211> 570

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC_FEATURE

<222> (1)..(570)

<400> 44

Phe Glu Ser Ser Pro Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser 1 5 10 15

Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val 20 25 30

Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly 35 40 45

Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala 50 55 60

Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe
70 75 80

Gly Asp Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp 85 90 95

Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu 100 105 110

Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile 115 120 125

Val Asp Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp 130 135 140

Gly His Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser 145 150 155 160

Lys Arg Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser 165 170 175

Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val
180 185 190

Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp 195 200 205

Glı	1 Ly: 210	s Thi	Gly	/ Le	ı Val	Ser 215	c Vai	l As _l	p Ası	Asp	220		r Gl	n Ly	s Gly	
Cys 225	s Cys	s Thr	Sei	r Pro	230	ı Asp	Gly	y Lei	ı Glr	1 Lys 235		a Lys	s Arg	g Ile	e Gly 240	
Phe	e Pro	Val	. Met	: Ile 245	Lys	. Ala	Sei	c Glu	250		Gly	/ Gly	y Lys	5 Gly 259	/ Ile	
Arg	Glr	ı Val	Glu 260	Arg	, Glu	Glu	Asp	265		Ala	Leu	ι Туг	His 270		n Ala	
Ala		Glu 275	Ile	Pro	Gly	Ser	Pro 280	o Ile	Phe	Ile	Met	Lys 285		ı Ala	Gly	
Arg	Ala 290	Arg	His	Leu	Glu	Val 295	Gln	Leu	Leu	Ala	Asp 300		Tyr	Gly	Thr	
Asn 305	Ile	Ser	Leu	Phe	Gly 310	Arg	Asp	Cys	Ser	Val 315	Gln	Arg	Arg	His	Gln 320	
Lys	Ile	Ile	Glu	Glu 325	Ala	Pro	Val	Thr	Ile 330	Ala	Lys	Ala	Glu	Thr 335	Phe	
His	Glu	Met	Glu 340	Lys	Ala	Ala	Val	Arg 345	Leu	Gly	Lys	Leu	Val 350	Gly	Tyr	
Val	Ser	Ala 355	Gly	Thr	Val	Glu	Tyr 360	Leu	Tyr	Ser	His	Asp 365	Asp	Gly	Lys	
Phe	Tyr 370	Phe	Leu	Glu	Leu	Asn 375	Pro	Arg	Leu	Gln	Val 380	Glu	His	Pro	Thr	
Thr 385	Glu	Met	Val	Ser	Gly 390	Val			Pro		Ala	Gln	Leu	Gln	Ile 400	
Ala	Met	Gly	Ile	Pro 405	Met	His	Arg	Ile	Ser 410	Asp	Ile	Arg	Thr	Leu 415	Tyr	
Gly	Met	Asn	Pro 420	His	Ser	Ala	Ser	Glu 425	Ile	Asp	Phe	Glu	Phe 430	Lys	Thr	
Gln	Asp	Ala 435	Thr	Lys	Lys	Gln .	Arg 440	Arg	Pro	Ile		Lys 445	Gly	His	Cys	

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His Lys Met Thr Ala Glu Lys Pro Asp <210> 45 <211> 560 <212> PRT Saccharomyces cerevisiae <213> <220> <221> MISC FEATURE (1)..(560) <222> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC domain (AAs 12-571) <400> 45 Gln Lys Met Glu Tyr Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile

Arg 65	g Sei	: Val	l Arg	J Lys	70) Ala	а Туз	r Glı	ı Thr	75	e Gly	y As _l	p Ası	o Arg	Thr 80	
Val	l Glr	n Ph∈	e Val	Ala 85	a Met	: Ala	Thi	r Pro	90	ı Ası	o Lei	ı Glı	ı Ala	a Asr 95	n Ala	
Glu	і Туг	: Ile	e Arg	Met	: Ala	ı Asp	Glr	1 Tyr 105		e Glı	ı Val	Pro	Gly 110	_	Thr	
Asn	Asn	Asn 115	Asn	Tyr	` Ala	Asn	Val		Leu	ılle	e Val	. Asp 125		e Ala	Glu	
Arg	130	Asp	Val	Asp	Ala	Val 135		Ala	Gly	Trp	Gly 140		a Ala	. Ser	Glu	
Asn 145	Pro	Leu	. Leu	Pro	Glu 150	Lys	Leu	Ser	Gln	Ser 155		Arg	Lys	Val	Ile 160	
Phe	Ile	Gly	Pro	Pro 165	Gly	Asn	Ala	Met	Arg 170		Leu	Gly	Asp	Lys 175	Ile	
Ser	Ser	Thr	Ile 180	Val	Ala	Gln	Ser	Ala 185		Val	Pro	Cys	Ile 190	Pro	Trp	
Ser	Gly	Thr 195	Gly	Val	Asp	Thr	Val 200		Val	Asp	Glu	Lys 205	Thr	Gly	Leu	
Val	Ser 210	Val	Asp	Asp	Asp	Ile 215	Tyr	Gln	Lys	Gly	Cys 220	Cys	Thr	Ser	Pro	
Glu 225	Asp	Gly	Leu	Gln	Lys 230	Ala	Lys	Arg	Ile	Gly 235	Phe	Pro	Val	Met	Ile 240	
Lys	Ala	Ser	Glu	Gly 245	Gly	Gly	Gly	Lys	Gly 250	Ile	Arg	Gln	Val	Glu 255	Arg	
Glu	Glu	Asp	Phe 260	Ile	Ala	Leu	Tyr	His 265	Gln	Ala	Ala	Asn	Glu 270	Ile	Pro	
Gly	Ser	Pro 275	Ile	Phe	Ile	Met	Lys 280	Leu	Ala	Gly	Arg	Ala 285	Arg	His	Leu	
Glu	Val 290	Gln	Leu	Leu	Ala	Asp 295	Gln	Tyr	Gly	Thr	Asn 300	Ile	Ser	Leu	Phe	

Gly 305		Asp	Cys	Ser	Val 310		Arg	Arg	His	Gln 315		Ile	· Ile	: Glu	Glu 320
Ala	Pro	Val	Thr	Ile 325		Lys	Ala	Glu	Thr 330		His	Glu	Met	Glu 335	Lys
Ala	Ala	Val	Arg 340		Gly	Lys	Leu	Val 345		Tyr	Val	Ser	Ala 350		Thr
Val	Glu	Tyr 355		Tyr	Ser	His	Asp 360		Gly	Lys	Phe	Tyr 365		Leu	Glu
Leu	Asn 370	Pro	Arg	Leu	Gln	Val 375		His	Pro	Thr	Thr 380	Glu	Met	Val	Ser
Gly 385	Val	Asn	Leu	Pro	Ala 390	Ala	Gln	Leu	Gln	Ile 395	Ala	Met	Gly	Ile	Pro 400
Met	His	Arg	Ile	Ser 405	Asp	Ile	Arg	Thr	Leu 410		Gly	Met	Asn ,	Pro 415	His
Ser	Ala	Ser	Glu 420	Ile	Asp	Phe	Glu	Phe 425	Lys	Thr	Gln	Asp	Ala 430	Thr	Lys
Lys	Gln	Arg 435	Arg	Pro	Ile	Pro	Lys 440	Gly	His	Cys	Thr	Ala 445	Cys	Arg	Ile
Thr	Ser 450	Glu	Asp	Pro	Asn	Asp 455	Gly	Phe	Lys	Pro	Ser 460	Gly	Gly	Thr	Leu
His 465	Glu	Leu	Asn	Phe	Arg 470	Ser	Ser	Ser	Asn	Val 475	Trp	Gly	Tyr	Phe	Ser 480
Val	Gly	Asn	Asn				His				Asp				Gly
His	Ile	Phe	Ala 500	Phe	Gly	Glu	Asn	Arg 505	Gln	Ala	Ser	Arg	Lys 510	His	Met
Val	Val	Ala 515	Leu	Lys	Glu	Leu	Ser 520	Ile	Arg	Gly	Asp	Phe 525	Arg	Thr	Thr
	Glu 530	Tyr	Leu	Ile	Lys	Leu 535	Leu	Glu	Thr	Glu	Asp 540	Phe	Glu	Asp	Asn
Thr	Ile	Thr	Thr	Gly	Trp	Leu	Asp	Asp	Leu	Ile	Thr	His	Lys	Met	Thr

<210> 46

<211> 550

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC_FEATURE

<222> (1)..(550)

<223> N- and C-terminal deleted Saccharomyces cerevisiae ACCase BC
domain (AAs 17-566)

<400> 46

Glu Ile Thr Asn Tyr Ser Glu Arg His Thr Glu Leu Pro Gly His Phe 1 5 10

Ile Gly Leu Asn Thr Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp 20 25 30

Phe Val Lys Ser His Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile 35 40 45

Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys 50 55

Trp Ala Tyr Glu Thr Phe Gly Asp Asp Arg Thr Val Gln Phe Val Ala 65 70 75 80

Met Ala Thr Pro Glu Asp Leu Glu Ala Asn Ala Glu Tyr Ile Arg Met 85 90 95

Ala Asp Gln Tyr Ile Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr 100 105 110

Ala Asn Val Asp Leu Ile Val Asp Ile Ala Glu Arg Ala Asp Val Asp 115 120 125

Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro 130 135 140

Glu Lys Leu Ser Gln Ser Lys Arg Lys Val Ile Phe Ile Gly Pro Pro 145 150 155 160

Gly Asn Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val 165 170 175

Ala	Gln	Ser	Ala 180	Lys	Val	Pro	Cys	Ile 185	Pro	Trp	Ser	Gly	Thr 190	Gly	Val
Asp	Thr	Val 195	His	Val	Asp	Glu	Lys 200	Thr	Gly	Leu	Val	Ser 205	Val	Asp	Asp
Asp	Ile 210	Tyr	Gln	Lys	Gly	Cys 215	Cys	Thr	Ser	Pro	Glu 220	Asp	Gly	Leu	Gln
Lys 225		Lys	Arg	Ile	Gly 230	Phe	Pro	Val	Met	Ile 235	Lys	Ala	Ser	Glu	Gly 240
Gly	Gly	Gly	Lys	Gly 245	Ile	Arg	Gln	Val	Glu 250	Arg	Glu	Glu	Asp	Phe 255	Ile
Ala	Leu	Tyr	His 260	Gln	Ala	Ala	Asn	Glu 265	Ile	Pro	Gly	Ser	Pro 270	Ile	Phe
Ile	Met	Lys 275	Leu	Ala	Gly	Arg	Ala 280	Arg	His	Leu	Glu	Val 285	Gln	Leu	Leu
Ala	Asp 290	Gln	Tyr	Gly	Thr	Asn 295	Ile	Ser	Leu	Phe	Gly 300	Arg	Asp	Cys	Ser
Val 305	Gln	Arg	Arg	His	Gln 310	Lys	Ile	Ile	Glu	Glu 315	Ala	Pro	Val	Thr	Ile 320
Ala	Lys	Ala	Glu	Thr 325	Phe	His	Glu	Met	Glu 330	Lys	Ala	Ala	Val	Arg 335	Leu
Gly	Lys	Leu	Val 340	Gly	Tyr	Val	Ser	Ala 345	Gly	Thr	Val	Glu	Tyr 350	Leu	Tyr
Ser	His	Asp 355	Asp	Gly	Lys	Phe	Tyr 360	Phe	Leu	Glu	Leu	Asn 365	Pro	Arg	Leu
Gln	Val 370	Glu	His	Pro	Thr	Thr 375	Glu	Met	Val	Ser	Gly 380	Val	Asn	Leu	Pro
Ala 385	Ala	Gln	Leu	Gln	Ile 390	Ala	Met	Gly	Ile	Pro 395	Met	His	Arg	Ile	Ser 400
Asp	Ile	Arg	Thr	Leu 405	Tyr	Gly	Met	Asn	Pro 410	His	Ser	Ala	Ser	Glu 415	Ile
Asp	Phe	Glu	Phe	Lys	Thr	Gln	Asp	Ala	Thr	Lys	Lys	Gln	Arg	Arg	Pro

Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro 435 440 445

Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe 450 455 460

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly 465 470 475 480

Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe 485 490 495

Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys 500 505 510

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 515 520 525

Lys Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly 530 540

Trp Leu Asp Asp Leu Ile 545 550

<210> 47

<211> 540

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(540)

<400> 47

Ser Glu Arg His Thr Glu Leu Pro Gly His Phe Ile Gly Leu Asn Thr 1 5 10 15

Val Asp Lys Leu Glu Glu Ser Pro Leu Arg Asp Phe Val Lys Ser His 20 25 30

Gly Gly His Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile 35 40 45

Ala	Ala 50	Val	Lys	Glu	Ile	Arg 55	Ser	Val	Arg	Lys	Trp	Ala	Tyr	Glu	Thr
Phe 65	Gly	Asp	Asp	Arg	Thr 70	Val	Gln	Phe	Val	Ala 75	Met	Ala	Thr	Pro	Glu 80
Asp	Leu	Glu	Ala	Asn 85	Ala	Glu	Tyr	Ile	Arg 90	Met	Ala	Asp	Gln	Tyr 95	Ile
Glu	Val	Pro	Gly 100	Gly	Thr	Asn	Asn	Asn 105	Asn	Tyr	Ala	Asn	Val 110	Asp	Leu
Ile	Val	Asp 115	Ile	Ala	Glu	Arg	Ala 120	Asp	Val	Asp	Ala	Val 125	Trp	Ala	Gly
Trp	Gly 130	His	Ala	Ser	Glu	Asn 135	Pro	Leu	Leu	Pro	Glu 140	Lys	Leu	Ser	Gln
Ser 145	Lys	Arg	Lys	Val	Ile 150	Phe	Ile	Gly	Pro	Pro 155	Gly	Asn	Ala	Met	Arg 160
Ser	Leu	Gly	Asp	Lys 165	Ile	Ser	Ser	Thr	Ile 170	Val	Ala	Gln	Ser	Ala 175	Lys
Val	Pro	Cys	Ile 180	Pro	Trp	Ser	Gly	Thr 185	Gly	Val	Asp	Thr	Val 190	His	Val
Asp	Glu	Lys 195	Thr	Gly	Leu	Val	Ser 200	Val	Asp	Asp	Asp	Ile 205	Tyr	Gln	Lys
Gly	Cys 210	Суз	Thr	Ser	Pro	Glu 215	Asp	Gly	Leu	Gln	Lys 220	Ala	Lys	Arg	Ile
Gly 225		Pro	Val	Met			Ala						Gly		Gly 240
Ile	Arg	Gln	Val	Glu 245	Arg	Glu	Glu	Asp	Phe 250	Ile	Ala	Leu	Tyr	His 255	Gln
Ala	Ala	Asn	Glu 260	Ile	Pro	Gly	Ser	Pro 265	Ile	Phe	Ile	Met	Lys 270	Leu	Ala
Gly	Arg	Ala 275	Arg	His	Leu	Glu	Val 280	Gln	Leu	Leu	Ala	Asp 285	Gln	Tyr	Gly
Thr	Asn	Ile	Ser	Leu	Phe	Gly	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His

Gln Lys Ile Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr

Phe His Glu Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly

Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro

Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln

Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu

Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys

Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His

Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys

Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn

Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe

Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln

Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg

Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr

Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp

- <210> 48
- <211> 545
- <212> PRT
- <213> Phytophthora infestans
- <220>
- <221> MISC_FEATURE
- <222> (1)..(545)
- <223> N-terminal deleted Phytophthora ACCase BC domain (AAs 11-555)
- <400> 48
- Asp Val Ala Ala Tyr Ala Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn 1 5 10 15
- Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro 20 25 30
- Ile Thr Ser Val Leu Ile Ala Asn Asn Gly Ile Ser Ala Val Lys Ala 35 40 45
- Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu Met Phe Ala Asp Glu His
 50 55 60
- Val Val Thr Phe Val Val Met Ala Thr Pro Glu Asp Leu Lys Ala Asn 65 70 75 80
- Ala Glu Tyr Ile Arg Met Ala Glu His Val Val Glu Val Pro Gly Gly 85 90 95
- Ser Asn Asn His Asn Tyr Ala Asn Val Ser Leu Ile Ile Glu Ile Ala 100 105 110
- Glu Arg Phe Asn Val Asp Ala Val Trp Ala Gly Trp Gly His Ala Ser 115 120 125
- Glu Asn Pro Leu Leu Pro Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile 130 135 140
- Val Phe Ile Gly Pro Pro Gly Lys Pro Met Arg Ala Leu Gly Asp Lys 145 150 155 160
- Ile Gly Ser Thr Ile Ile Ala Gln Ser Ala Lys Val Pro Thr Ile Ala 165 170 175
- Trp Asn Gly Asp Gly Met Glu Val Asp Tyr Lys Glu His Asp Gly Ile 180 185 190

Pro) Asp	9 Glu 195	ı Ile	: Туг	Asn	ı Ala	Ala 200		: Leu	ı Arg	Asp	Gly 205		n His	s Cys
Leu	Asp 210	Glu	ı Cys	Lys	a Arg	1le 215		Phe	Pro	Val	Met 220		Lys	: Ala	Ser
Glu 225	Gly	Gly	gly	· Gly	Lys 230		'Ile	Arg	Met	Val 235		Glu	. Glu	Ser	Gln 240
Val	Leu	Ser	· Ala	Trp 245		Ala	Val	Arg	Gly 250		Ile	Pro	Gly	Ser 255	Pro
Ile	Phe	Val	Met 260	Lys	Leu	Ala	Pro	Lys 265		Arg	His	Leu	Glu 270		Gln
Leu	Leu	Ala 275	Asp	Thr	Tyr	Gly	Asn 280		Ile	Ala	Leu	Ser 285	Gly	Arg	Asp
Cys	Ser 290	Val	Gln	Arg	Arg	His 295	Gln	Lys	Ile	Val	Glu 300	Glu	Gly	Pro	Val
Leu 305	Ala	Pro	Thr	Gln	Glu 310	Val	Trp	Glu	Lys	Met 315	Met	Arg	Ala	Ala	Thr 320
Arg	Leu	Ala	Gln	Glu 325	Val	Glu	Tyr	Val	Asn 330	Ala	Gly	Thr	Val	Glu 335	Tyr
Leu	Phe	Ser	Glu 340	Leu	Pro	Glu	Asp	Asn 345	Gly	Asn	Ser	Phe	Phe 350	Phe	Leu
Glu	Leu	Asn 355	Pro	Arg	Leu	Gln	Val 360	Glu	His	Pro	Val	Thr 365	Glu	Met	Ile
Thr	His 370	Val	Asn	Leu	Pro		Ala				Val 380	Ala	Met	Gly	Ile
Pro 385	Leu	His	Cys	Ile	Pro 390	Asp	Val	Arg	Arg	Leu 395	Tyr	Asn	Lys	Asp	Ala 400
Phe	Glu	Thr	Thr	Val 405	Ile	Asp	Phe		Ala 410	Glu	Lys	Gln		Pro 415	Pro
His	Gly	His	Val 420	Ile	Ala	Ala		Ile 425	Thr	Ala	Glu .		Pro 430	Asn	Ala

Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser 435 440 445 Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val 450 455 460 His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro 465 470 475 480 Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu 485 490 495 Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met 500 505 510 Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu 515 520 525 Asp Glu Arg Ile Ser His His Asn Glu Val Arg Leu Gln Gly Arg Pro 530 535 540 Asp 545 <210> 49 <211> 535 <212> PRT Phytophthora infestans <213> <220> <221> MISC_FEATURE <222> (1)..(535) N-terminal deleted Phytophthora ACCase BC domain (AAs 21-555) <400> 49 Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu 1 5 10 15 Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile Ala Asn Asn Gly 20 Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu 35 40 45 Met Phe Ala Asp Glu His Val Val Thr Phe Val Val Met Ala Thr Pro

60

55

Glu 65	Asp	Leu	Lys	Ala	Asn 70	Ala	Glu	Tyr	· Ile	Arg 75	, Met	Ala	Glu	His	Val 80	
Val	Glu	. Val	Pro	Gly 85	Gly	Ser	Asn	. Asn	His 90	Asn	Tyr	Ala	Asn	Val 95	Ser	
Leu	Ile	Ile	Glu 100		Ala	Glu	Arg	Phe 105		Val	Asp	Ala	Val 110	_	Ala	
Gly	Trp	Gly 115	His	Ala	Ser	Glu	Asn 120		Leu	Leu	. Pro	Asp 125		Leu	Ala	
Gln	Thr 130	Glu	Arg	Lys	Ile	Val 135	Phe	Ile	Gly	Pro	Pro 140		Lys	Pro	Met	
Arg 145	Ala	Leu	Gly	Asp	Lys 150	Ile	Gly	Ser	Thr	Ile 155	Ile	Ala	Gln	Ser	Ala 160	
Lys	Val	Pro	Thr	Ile 165	Ala	Trp	Asn	Gly	Asp 170		Met	Glu	Val	Asp 175	Tyr	
Lys	Glu	His	Asp 180	Gly	Ile	Pro	Asp	Glu 185	Ile	Tyr	Asn	Ala	Ala 190	Met	Leu	
Arg	Asp	Gly 195	Gln	His	Cys	Leu	Asp 200	Glu	Cys	Lys	Arg	Ile 205	Gly	Phe	Pro	
Val	Met 210	Ile	Lys	Ala	Ser	Glu 215	Gly	Gly	Gly	Gly	Lys 220	Gly	Ile	Arg	Met	
Val 225	His	Glu	Glu	Ser	Gln 230	Val	Leu	Ser	Ala	Trp 235	Glu	Ala	Val	Arg	Gly 240	
Glu	Ile	Pro	Gly		Pro						Leu			Lys 255	Ser	
Arg	His	Leu	Glu 260	Val	Gln	Leu	Leu	Ala 265	Asp	Thr	Tyr	Gly	Asn 270	Ala	Ile	
Ala	Leu	Ser 275	Gly	Arg	Asp		Ser 280	Val	Gln	Arg	Arg	His 285	Gln	Lys	Ile	
Val	Glu 290	Glu	Gly	Pro		Leu 295	Ala	Pro	Thr	Gln	Glu 300	Val	Trp	Glu	Lys	

Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly Asn Ser Phe Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His His Asn Glu Val

Arg Leu Gln Gly Arg Pro Asp

<210> 50

- <211> 545
- <212> PRT
- <213> Phytophthora infestans
- <220>
- <221> MISC FEATURE
- <222> (1)..(545)
- <223> C-terminal deleted Phytophthora ACCase BC domain (AAs 1-545)
- <400> 50
- Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala 1 5 10 15
- Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu 20 25 30
- Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile 35 40 45
- Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser 50 55 60
- Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val 65 70 75 80
- Met Ala Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Arg Met 85 90 95
- Ala Glu His Val Val Glu Val Pro Gly Gly Ser Asn Asn His Asn Tyr 100 105 110
- Ala Asn Val Ser Leu Ile Ile Glu Ile Ala Glu Arg Phe Asn Val Asp 115 120 125
- Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Leu Leu Pro 130 135 140
- Asp Thr Leu Ala Gln Thr Glu Arg Lys Ile Val Phe Ile Gly Pro Pro 145 150 155
- Gly Lys Pro Met Arg Ala Leu Gly Asp Lys Ile Gly Ser Thr Ile Ile 165 170 175
- Ala Gln Ser Ala Lys Val Pro Thr Ile Ala Trp Asn Gly Asp Gly Met 180 185 190
- Glu Val Asp Tyr Lys Glu His Asp Gly Ile Pro Asp Glu Ile Tyr Asn

195 200 205

Ala	Ala 210	Met	Leu	Arg	Asp	Gly 215	Gln	His	Cys	Leu	Asp 220	Glu	Cys	Lys	Arg
Ile 225	Gly	Phe	Pro	Val	Met 230	Ile	Lys	Ala	Ser	Glu 235	Gly	Gly	Gly	Gly	Lys 240
Gly	Ile	Arg	Met	Val 245	His	Glu	Glu	Ser	Gln 250	Val	Leu	Ser	Ala	Trp 255	Glu
Ala	Val	Arg	Gly 260	Glu	Ile	Pro	Gly	Ser 265	Pro	Ile	Phe	Val	Met 270	Lys	Leu
Ala	Pro	Lys 275	Ser	Arg	His	Leu	Glu 280	Val	Gln	Leu	Leu	Ala 285	Asp	Thr	Tyr
Gly	Asn 290	Ala	Ile	Ala	Leu	Ser 295	Gly	Arg	Asp	Cys	Ser 300	Val	Gln	Arg	Arg
His 305	Gln	Lys	Ile	Val	Glu 310	Glu	Gly	Pro	Val	Leu 315	Ala	Pro	Thr	Gln	Glu 320
			Lys	325					330					335	
			Asn 340					345					350		
		355	Gly				360					365			
	370		His	_		375					380				
385			Leu		390					395			-		400
Asp	val	arg	Arg	Leu 405	Tyr	Asn	гÀг	Asp	A1a 410	Phe	GLu	Thr	Thr	Val 415	TTE

Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala

Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser

Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr Ser Trp Leu Asp Glu Arg Ile Ser His His <210> <211> <212> PRT <213> Phytophthora infestans <220> <221> MISC_FEATURE <222> (1)..(535) C-terminal deleted Phytophthora ACCase BC domain (AAs 1-535) <400> 51 Met Val Ala Glu Glu Ala Pro Pro Ala Ala Asp Val Ala Ala Tyr Ala Glu Thr Arg Ser Asp Ser Asn Pro Leu Asn Tyr Ala Ser Met Glu Glu Tyr Val Arg Leu Gln Lys Gly Thr Arg Pro Ile Thr Ser Val Leu Ile Ala Asn Asn Gly Ile Ser Ala Val Lys Ala Ile Arg Ser Ile Arg Ser Trp Ser Tyr Glu Met Phe Ala Asp Glu His Val Val Thr Phe Val Val

Met	Ala	Thr	Pro	85	Asp	Leu	гуs	Ala	90	Ala	Glu	Tyr	ile	95	Met
Ala	Glu	His	Val 100	Val	Glu	Val	Pro	Gly 105	Gly	Ser	Asn	Asn	His 110	Asn	Tyr
Ala	Asn	Val 115	Ser	Leu	Ile	Ile	Glu 120	Ile	Ala	Glu	Arg	Phe 125	Asn	Val	Asp
Ala	Val 130	Trp	Ala	Gly	Trp	Gly 135	His	Ala	Ser	Glu	Asn 140	Pro	Leu	Leu	Pro
Asp 145	Thr	Leu	Ala	Gln	Thr 150	Glu	Arg	Lys	Ile	Val 155	Phe	Ile	Gly	Pro	Pro 160
Gly	Lys	Pro	Met	Arg 165	Ala	Leu	Gly	Asp	Lys 170	Ile	Gly	Ser	Thr	Ile 175	Ile
Ala	Gln	Ser	Ala 180	Lys	Val	Pro	Thr	Ile 185	Ala	Trp	Asn	Gly	Asp 190	Gly	Met
Glu	Val	Asp 195	Tyr	Lys	Glu	His	Asp 200	Gly	Ile	Pro	Asp	Glu 205	Ile	Tyr	Asn
Ala	Ala 210	Met	Leu	Arg	Asp	Gly 215	Gln	His	Cys	Leu	Asp 220	Glu	Cys	Lys	Arg
Ile 225	Gly	Phe	Pro	Val	Met 230	Ile	Lys	Ala	Ser	Glu 235	Gly	Gly	Gly	Gly	Lys 240
Gly	Ile	Arg	Met	Val 245	His	Glu	Glu	Ser	Gln 250	Val	Leu	Ser	Ala	Trp 255	Glu
Ala	Val	Arg	Gly 260	Glu	Ile	Pro	Gly	Ser 265	Pro	Ile	Phe	Val	Met 270	Lys	Leu
Ala	Pro	Lys 275	Ser	Arg	His	Leu	Glu 280	Val	Gln	Leu	Leu	Ala 285	Asp	Thr	Tyr
Gly	Asn 290	Ala	Ile	Ala	Leu	Ser 295	Gly	Arg	Asp	Cys	Ser 300	Val	Gln	Arg	Arg
His	Gln	Lys	Ile	Val	Glu	Glu	Gly	Pro	Val	Leu	Ala	Pro	Thr	Gln	Glu

Val Trp Glu Lys Met Met Arg Ala Ala Thr Arg Leu Ala Gln Glu Val Glu Tyr Val Asn Ala Gly Thr Val Glu Tyr Leu Phe Ser Glu Leu Pro Glu Asp Asn Gly Asn Ser Phe Phe Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Met Ile Thr His Val Asn Leu Pro Ala Ala Gln Leu Gln Val Ala Met Gly Ile Pro Leu His Cys Ile Pro Asp Val Arg Arg Leu Tyr Asn Lys Asp Ala Phe Glu Thr Thr Val Ile Asp Phe Asp Ala Glu Lys Gln Lys Pro Pro His Gly His Val Ile Ala Ala Arg Ile Thr Ala Glu Asp Pro Asn Ala Gly Phe Gln Pro Thr Ser Gly Ala Ile Gln Glu Leu Asn Phe Arg Ser Thr Pro Asp Val Trp Gly Tyr Phe Ser Val Asp Ser Ser Gly Gln Val His Glu Phe Ala Asp Ser Gln Ile Gly His Leu Phe Ser Trp Ser Pro Thr Arg Glu Lys Ala Arg Lys Asn Met Val Leu Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Ile His Thr Thr Val Glu Tyr Ile Val Asn Met Met Glu Ser Asp Asp Phe Lys Tyr Asn Arg Ile Ser Thr

<210> 52

<211> 581

<212> PRT

<213> Magnaporthe grisea

- <220>
- <221> MISC_FEATURE
- <222> (1)..(581)
- <223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 12-592
- <400> 52
- Asn Ser Ser Arg Gln Arg Asn Gly Ala Asn Gly Val Thr Val Pro Val 1 5 10 15
- Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg His Lys Ile Ala Asp His 20 25 30
- Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala Pro Pro Ser Lys Val Lys
 35 40 45
- Glu Trp Val Ala Ala His Asp Gly His Thr Val Ile Thr Asn Val Leu 50 55
- Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile Arg Ser Val Arg 65 70 75 80
- Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr 85 90 95
- Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg 100 105 110
- Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn 115 120 125
- Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu Arg Met Asn Val 130 135 140
- His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu 145 150 155 160
- Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro 165 170 175
- Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile 180 185 190
- Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp Ser Gly Thr Gly
 195 200 205

Val	Asp 210	Ala	a V	al (3ln	Ile	Asp 215	Lys	Lys	Gly	Ile	Val ' 220	Thr	Val 2	Asp 2	Asp
Asp 225	Thr	Туз	c A	la 1		Gly 230	Cys	Val	Thr	Ser	Trp 235	Gln	Glu	Gly	Leu	Glu 240
Lys	Ala	Arg	g G		Ile 245	Gly	Phe	Pro	Val	Met 250	Ile	Lys	Ala	Ser	Glu 255	Gly
Gly	Gly	Gl		760 Jàs	Gly	Ile	Arg	Lys	Ala 265	Val	Ser	Glu	Glu	Gly 270	Phe	Glu
Glu	Leu	Ту 27		ŗÀa	Ala	Ala	Ala	Ser 280	Glu	Ile	Pro	Gly	Ser 285	Pro	Ile	Phe
Ile	Met 290		s 1	Lėu	Ala	Gly	Asn 295		Arg	His	Leu	Glu 300	Val	Gln	Leu	Leu
Ala 305		G1	.n '	Tyr	Gly	Asn 310		Ile	Ser	Leu	Phe 315	Gly	Arg	Asp	Cys	Ser 320
Val	Glr	n Ar	g	Arg	His 325	Gln	Lys	: Ile	Ile	Glu 330	Glu	Ala	Pro	Val	Thr 335	Ile
Ala	ı Ly:	s Pi		Asp 340	Thr	Phe	Lys	s Ala	Met 345	Glu	Glu	Ala	Ala	Val 350	Arg	Leu
Glγ	/ Ar		eu 55	Val	Gly	Tyr	· Val	l Ser 360	r Ala	d Gly	Thr	Val	Glu 365	Tyr	Leu	Tyr
Sei	r Hi 37		la	Asp	Asp	Lys	37!	e Туі 5	c Phe	e Lev	ı Glu	1 Leu 380	. Asn	Pro	Arg	Leu
Gl:		l G	lu	His	Pro	390	r Th	r Glı	ı Gly	y Val	Sei 395	Gly	Val	. Asn	Leu	Pro 400
Al	a Se	r G	ln	Leu	Glr 405		e Al	a Me	t Gl	y Ile 410	e Pro	o Lev	ı His	arg	Ile 415	s Ser
As	p Il	e A	rg	Leu 420		ı Ту:	r Gl	y Va	1 As; 42	p Pro 5	o Ly:	s Lei	ı Sei	Thr 430	Glu	ı Ile
As	p Pł		sp 135		e Ly:	s As:	n Pr	o As 44	p Se 0	r Gl	u Ly	s Thi	c Gl: 44!	n Arg	g Arg	g Pro
Se	r Pi	co I	Lys	Gly	y Hi	s Le	u Th	ır Al	а Су	s Ar	g Il	e Th	r Se	r Glu	ı Ası	p Pro

450 455 460

Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His Glu Leu Asn Phe 470 475 480

Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly
485
490
495

Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr 500 505 510

Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys 515 520 525

Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile 530 540

Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly 545 550 560

Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala Glu Arg Pro Asp 565 570 575

Lys Met Leu Ala Val 580

<210> 53

<211> 571

<212> PRT

<213> Magnaporthe grisea

<220>

<221> MISC FEATURE

<222> (1)..(571)

<223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 22-591)

<400> 53

Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr Tyr Ala Gln Arg
1 5 10 15

His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg Leu Glu Asn Ala 20 25 30

Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His Asp Gly His Thr 35 40 45

Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu

Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala

Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly

Gly Thr Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val

Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala

Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys

Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp

Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile

Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly

Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser

Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met

Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Ala Val

Ser Glu Glu Glu Glu Leu Tyr Lys Ala Ala Ser Glu Ile

Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His

Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu

Phe Gl 305	y Arg	Asp	Cys	Ser 310	Val	Gln	Arg	Arg	His 315	Gln	Lys	Ile	Ile	Glu 320
Glu Al	a Pro	Val	Thr 325	Ile	Ala	Lys	Pro	Asp 330	Thr	Phe	Lys	Ala	Met 335	Glu
Glu Al	a Ala	Val 340	Arg	Leu	Gly	Arg	Leu 345	Val	Gly	Tyr	Val	Ser 350	Ala	Gly
Thr Va	1 Glu 355	-	Leu	Tyr	Ser	His 360	Ala	Asp	Asp	Lys	Phe 365	Tyr	Phe	Leu
Glu Le 37		Pro	Arg	Leu	Gln 375	Val	Glu	His	Pro	Thr 380	Thr	Glu	Gly	Val
Ser Gl 385	y Val	Asn	Leu	Pro 390	Ala	Ser	Gln	Leu	Gln 395	Ile	Ala	Met	Gly	Ile 400
Pro Le	u His	Arg	Ile 405	Ser	Asp	Ile	Arg	Leu 410	Leu	Tyr	Gly	Val	Asp 415	Pro
Lys Le	u Ser	Thr 420	Glu	Ile	Asp	Phe	Asp 425	Phe	Lys	Asn	Pro	Asp 430	Ser	Glu
Lys Th	r Gln 435	_	Arg	Pro	Ser	Pro 440	Lys	Gly	His	Leu	Thr 445	Ala	Cys	Arg
Ile Th		Glu	Asp	Pro	Gly 455	Glu	Gly	Phe	Lys	Pro 460	Ser	Asn	Gly	Val
Met Hi 465	s Glu	Leu	Asn	Phe 470	Arg	Ser	Ser	Ser	Asn 475	Val	Trp	Gly	Tyr	Phe 480
Ser Va	l Gly	Thr	Gln 485	Gly	Gly	Ile	His	Ser 490	Phe	Ser	Asp	Ser	Gln 495	Phe
Gly Hi	s Ile	Phe 500	Ala	Tyr	Gly	Glu	Asn 505	Arg	Ser	Ala	Ser	Arg 510	Lys	His
Met Va	l Ile 515		Leu	Lys	Glu	Leu 520	Ser	Ile	Arg	Gly	Asp 525	Phe	Arg	Thr
Thr Va		Tyr	Leu	Ile	Lys 535	Leu	Leu	Glu	Thr	Glu 540	Ala	Phe	Glu	Glu

Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu 545 550 555 560

Thr Ala Glu Arg Pro Asp Lys Met Leu Ala Val 565 570

- <210> 54
- <211> 581
- <212> PRT
- <213> Magnaporthe grisea
- <220>
- <221> MISC FEATURE
- <222> (1)..(581)
- <223> C-terminal deleted Magnaporthe ACCase (AAs 2-582)
- <400> 54

Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg

1 10 15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr 20 25 30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg
40
45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His
50 55 60

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile
70 75 80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr 85 90 95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu
100 105 110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val 115 120 125

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu 130 135 140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly145150150155

Trp	Gly	His	Ala	Ser 165	Glu	Asn	Pro	Lys	Leu 170	Pro	Glu	Ser	Leu	Ala 175	Ala
Ser	Pro	Lys	Lys 180	Ile	Ile	Phe	Ile	Gly 185	Pro	Pro	Gly	Ser	Ala 190	Met	Arg
Ser	Leu	Gly 195	Asp	Lys	Ile	Ser	Ser 200	Thr	Ile	Val	Ala	Gln 205	His	Ala	Gln
Val	Pro 210	Cys	Ile	Pro	Trp	Ser 215	Gly	Thr	Gly	Val	Asp 220	Ala	Val	Gln	Ile
Asp 225	Lys	Lys	Gly	Ile	Val 230	Thr	Val	Asp	Asp	Asp 235	Thr	Tyr	Ala	Lys	Gly 240
Cys	Val	Thr	Ser	Trp 245	Gln	Glu	Gly	Leu	Glu 250	Lys	Ala	Arg	Gln	Ile 255	Gly
Phe	Pro	Val	Met 260	Ile	Lys	Ala	Ser	Glu 265	Gly	Gly	Gly	Gly	Lys 270	Gly	Ile
Arg	Lys	Ala 275	Val	Ser	Glu	Glu	Gly 280	Phe	Glu	Glu	Leu	Tyr 285	Lys	Ala	Ala
Ala	Ser 290	Glu	Ile	Pro	Gly	Ser 295	Pro	Ile	Phe	Ile	Met 300	Lys	Leu	Ala	Gly
Asn 305	Ala	Arg	His	Leu	Glu 310	Val	Gln	Leu	Leu	Ala 315	Asp	Gln	Tyr	Gly	Asn 320
Asn	Ile	Ser	Leu	Phe 325	Gly	Arg	Asp	Cys	Ser 330	Val	Gln	Arg	Arg	His 335	Gln
Lys	Ile	Ile			Ala					Ala	_		Asp 350		Phe
Lys	Ala	Met 355	Glu	Glu	Ala	Ala	Val 360	Arg	Leu	Gly	Arg	Leu 365	Val	Gly	Tyr
Val	Ser 370	Ala	Gly	Thr	Val	Glu 375	Tyr	Leu	Tyr	Ser	His 380	Ala	Asp	Asp	Lys
Phe 385	Tyr	Phe	Leu	Glu	Leu 390	Asn	Pro	Arg	Leu	Gln 395	Val	Glu	His	Pro	Thr 400

•

Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr <210> 55 <211> <212> PRT <213> Magnaporthe grisea <220> <221> MISC_FEATURE <222> (1)..(571) <223> C-terminal deleted Magnaporthe ACCase BC domain (AAs 2-572)

<400> 55

Thr Glu Thr Asn Gly Thr Ala Ala Ala Ala Asn Ser Ser Arg Gln Arg

1 10 15

Asn Gly Ala Asn Gly Val Thr Val Pro Val Ala Asn Gly Lys Ala Thr 20 25 30

Tyr Ala Gln Arg His Lys Ile Ala Asp His Phe Ile Gly Gly Asn Arg
35 40 45

Leu Glu Asn Ala Pro Pro Ser Lys Val Lys Glu Trp Val Ala Ala His 50

Asp Gly His Thr Val Ile Thr Asn Val Leu Ile Ala Asn Asn Gly Ile
65 70 75 80

Ala Ala Val Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr 85 90 95

Phe Gly Asp Glu Arg Ala Ile Gln Phe Thr Val Met Ala Thr Pro Glu 100 105 110

Asp Leu Gln Ala Asn Ala Asp Tyr Ile Arg Met Ala Asp His Tyr Val

Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu 130 135 140

Ile Val Asp Val Ala Glu Arg Met Asn Val His Ala Val Trp Ala Gly
145 150 155 160

Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala 165 170 175

Ser Pro Lys Lys Ile Ile Phe Ile Gly Pro Pro Gly Ser Ala Met Arg 180 185 190

Ser Leu Gly Asp Lys Ile Ser Ser Thr Ile Val Ala Gln His Ala Gln 195 200 205

Val Pro Cys Ile Pro Trp Ser Gly Thr Gly Val Asp Ala Val Gln Ile 210 215 220

Asp Lys Lys Gly Ile Val Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly 225 230 230

Cys Val Thr Ser Trp Gln Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly

245	250	255
745	250	7,77
2 1 3		

Ė	ne	Pro	vai	260	ite	гуѕ	Ala	ser	265	GTÅ	GIÀ	GIÀ	GIA	Lуs 270	GIÀ	ite
7	Arg	Lys	Ala 275	Val	Ser	Glu	Glu	Gly 280	Phe	Glu	Glu	Leu	Tyr 285	Lys	Ala	Ala
I	Ala	Ser 290	Glu	Ile	Pro	Gly	Ser 295	Pro	Ile	Phe	Ile	Met 300	Lys	Leu	Ala	Gly
	Asn 305	Ala	Arg	His	Leu	Glu 310	Val	Gln	Leu	Leu	Ala 315	Asp	Gln	Tyr	Gly	Asn 320
I	Asn	Ile	Ser	Leu	Phe 325	Gly	Arg	Asp	Cys	Ser 330	Val	Gln	Arg	Arg	His	Gln
1	ŗÀa	Ile	Ile	Glu 340	Glu	Ala	Pro	Val	Thr 345	Ile	Ala	Lys	Pro	Asp 350	Thr	Phe
I	ŗÀa	Ala	Met 355	Glu	Glu	Ala	Ala	Val 360	Arg	Leu	Gly	Arg	Leu 365	Val	Gly	Tyr
		370		-			Glu 375					380				
1.3	385	-				390	Asn				395					400
			_		405	_	Val			410					415	
			-	420			His		425					430		
(зтХ	Val	Asp 435	Pro	Lys	Leu	Ser	Thr 440	GLu	ITe	Asp	Phe	Asp 445	Phe	ьуз	Asn

Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val
485 490 495

Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu

Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro

Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr Ile Thr Thr Gly Trp <210> 56 <211> 622 <212> PRT <213> Homo sapiens <220> MISC FEATURE <221> <222> (1)..(622) C-terminal deleted Human ACCasel BC domain (AAs 1-622) <400> 56 Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Lys Asn Gly Ile Ala Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Val Asn Asn Ala Asp Asp Phe Pro Asn Leu Phe Arg Gln Val Gln Ala Glu Val Pro Gly Ser Pro Ile Phe Val Met Arg Leu Ala

Lys	Gln	Ser 355	Arg	His	Leu	Glu	Val 360	Gln	Ile	Leu	Ala	Asp 365	Gln	Tyr	Gly
Asn	Ala 370	Ile	Ser	Leu	Phe	Gly 375	Arg	Asp	Cys	Ser	Val 380	Gln	Arg	Arg	His
Gln 385	Lys	Ile	Ile	Glu	Glu 390	Ala	Pro	Ala	Thr	Ile 395	Ala	Thr	Pro	Ala	Val 400
Phe	Glu	His	Met	Glu 405	Gln	Cys	Ala	Val	Lys 410	Leu	Ala	Lys	Met	Val 415	Gly
Tyr	Val	Ser	Ala 420	Gly	Thr	Val	Glu	Tyr 425	Leu	Tyr	Ser	Gln	Asp 430	Gly	Ser
Phe	Tyr	Phe 435	Leu	Glu	Leu	Asn	Pro 440	Arg	Leu	Gln	Val	Glu 445	His	Pro	Cys
Thr	Glu 450	Met	Val	Ala	Asp	Val 455	Asn	Leu	Pro	Ala	Ala 460	Gln	Leu	Gln	Ile
Ala 465	Met	Gly	Ile	Pro	Leu 470	Tyr	Arg	Ile	Lys	Asp 475	Ile	Arg	Met	Met	Tyr 480
Gly	Val	Ser	Pro	Trp 485	Gly	Asp	Ser	Pro	Ile 490	Asp	Phe	Glu	Asp	Ser 495	Ala
His	Val	Pro	Суs 500	Pro	Arg	Gly	His	Val 505	Ile	Ala	Ala	Arg	Ile 510	Thr	Ser
Glu	Asn	Pro 515	Asp	Glu	Gly	Phe	Lys 520	Pro	Ser	Ser	Gly	Thr 525	Val	Gln	Glu
Leu	Asn 530	Phe	Arg	Ser	Asn	Lys 535	Asn	Val	Trp	Gly	Tyr 540	Phe	Ser	Val	Ala
Ala 545	Ala	Gly	Gly	Leu	His 550	Glu	Phe	Ala	Asp	Ser 555	Gln	Phe	Gly	His	Cys 560
Phe	Ser	Trp	Gly	Glu 565	Asn	Arg	Glu	Glu	Ala 570	Ile	Ser	Asn	Met	Val 575	Val
Ala	Leu	Lys	Glu 580	Leu	Ser	Ile	Arg	Gly 585	Asp	Phe	Arg	Thr	Thr 590	Val	Glu

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile 595 600 605

Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln 610 620

<210> 57

<211> 612

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(612)

<223> C-terminal deleted Human ACCase1 BC domain (AAs 1-612)

<400> 57

Met Asp Glu Pro Ser Pro Leu Ala Gln Pro Leu Glu Leu Asn Gln His

1 10 15

Ser Arg Phe Ile Ile Gly Ser Val Ser Glu Asp Asn Ser Glu Asp Glu 20 25 30

Ile Ser Asn Leu Val Lys Leu Asp Leu Leu Glu Glu Lys Glu Gly Ser 35 40 45

Leu Ser Pro Ala Ser Val Gly Ser Asp Thr Leu Ser Asp Leu Gly Ile 50 55 60

Ser Ser Leu Gln Asp Gly Leu Ala Leu His Ile Arg Ser Ser Met Ser 65 70 75 80

Gly Leu His Leu Val Lys Gln Gly Arg Asp Arg Lys Lys Ile Asp Ser 85 90 95

Gln Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe 100 105 110

Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile 115 120 125

Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met 130 135 140

Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu 145 150 155 160

Asp	Leu	Lys	Ala	Asn 165	Ala	Glu	Tyr	Ile :	Lys 170	Met .	Ala i	Asp	His	Tyr 175	Val
Pro	Val	Pro	Gly 180	Gly	Pro	Asn	Asn .	Asn 185	Asn	Tyr	Ala	Asn	Val 190	Glu	Leu
Ile	Leu	Asp 195	Ile	Ala	Lys	Arg	Ile 200	Pro	Val	Gln	Ala	Val 205	Trp	Ala	Gly
Trp	Gly 210	His	Ala	Ser	Glu	Asn 215	Pro	Lys	Leu	Pro	Glu 220	Leu	Leu	Leu	Lys
Asn 225	Gly	Ile	Ala	Phe	Met 230	Gly	Pro	Pro	Ser	Gln 235	Ala	Met	Trp	Ala	Leu 240
Gly	Asp	Lys	Ile	Ala 245	Ser	Ser	Ile	Val	Ala 250	Gln	Thr	Ala	Gly	Ile 255	Pro
Thr	Leu	Pro	Trp 260		Gly	Ser	Gly	Leu 265	Arg	Val	Asp	Trp	Gln 270	Glu	Asn
Asp	Phe	Ser 275		Arg	Ile	Leu	Asn 280	Val	Pro	Gln	Glu	Leu 285	Tyr	Glu	Lys
Gly	7 Tyr 290		. Lys	s Asp	Val	Asp 295	Asp	Gly	Leu	Lys	Ala 300	Ala	Glu	Glu	Val
Gl ₃		r Pro	va]	L Met	; Ile 310		Ala	Ser	Glu	Gly 315	Gly	Gly	· Gly	Lys	Gly 320
Ile	e Arç	J Ly:	s Val	l Asr 325		. Ala	Asp	Asp	9he	e Pro	Asn	Leu	Phe	Arg 335	Gln
Va:	l Gli	n Ala	a Gli 34	u Val	L Pro	Gly	/ Ser	Pro 345	o Il∈	e Phe	· Val	Met	350	Leu	Ala
Ly	s Gl	n Se 35		g Hi	s Lei	ı Glı	1 Val 360	. Glr	ı Ile	e Leu	ı Ala	Asr 365	Glr	туг	Gly
As	n Al 37		e Se	r Le	u Phe	e Gly 37		J Asp	о Суя	s Sei	7 Val 380	Glr	n Arg	g Arg	J His
Gl 38		s Il	e Il	e Gl	u Gli 39		a Pro	o Ala	a Thi	r Ile 395	e Ala	a Thi	r Pro	o Ala	a Val 400

Phe Glu His Met Glu Gln Cys Ala Val Lys Leu Ala Lys Met Val Gly

405 410 415

Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser 420 425 430

Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys 435 440 445

Thr Glu Met Val Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile 450 455 460

Ala Met Gly Ile Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr 465 470 475 480

Gly Val Ser Pro Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala 485 490 495

His Val Pro Cys Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser 500 505 510

Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu 515 520 525

Leu Asn Phe Arg Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala 530 540

Ala Ala Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys
550 555 560

Phe Ser Trp Gly Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val 565 570 575

Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu
580 585 590

Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile 595 600 605

Asp Thr Gly Trp 610

<210> 58

<211> 522

<212> PRT

<213> Homo sapiens

- <220>
- <221> MISC_FEATURE
- <222> (2)..(632)
- <223> N- and C-terminal deleted Human ACCase1 (AAs 102-622)

<400> 58

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys
1 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 20 25 30

Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 70 75 80

Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile 85 90 95

Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala 115 120 125

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile 130 135 140

Ala Ser Ser Ile Val Ala Gln Thr Ala Gly Ile Pro Thr Leu Pro Trp 145 150 155 160

Ser Gly Ser Gly Leu Arg Val Asp Trp Gln Glu Asn Asp Phe Ser Lys 165 170 175

Arg Ile Leu Asn Val Pro Gln Glu Leu Tyr Glu Lys Gly Tyr Val Lys 180 185 190

Asp Val Asp Asp Gly Leu Lys Ala Ala Glu Glu Val Gly Tyr Pro Val 195 200 205

Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys Val 210 215 220

Asn 225	Asn	Ala	Asp	Asp	Phe 230	Pro	Asn	Leu	Phe	Arg 235	Gln	Val	Gln	Ala	Glu 240
Val	Pro	Gly	Ser	Pro 245	Ile	Phe	Val	Met	Arg 250	Leu	Ala	Lys	Gln	Ser 255	Arg
His	Leu	Glu	Val 260	Gln	Ile	Leu	Ala	Asp 265	Gln	Tyr	Gly	Asn	Ala 270	Ile	Ser
Leu	Phe	Gly 275	Arg	Asp	Cys	Ser	Val 280	Gln	Arg	Arg	His	Gln 285	Lys	Ile	Ile
Glu	Glu 290	Ala	Pro	Ala	Thr	Ile 295	Ala	Thr	Pro	Ala	Val 300	Phe	Glu	His	Met
Glu 305	Gln	Cys	Ala	Val	Lys 310	Leu	Ala	Lys	Met	Val 315	Gly	Tyr	Val	Ser	Ala 320
Gly	Thr	Val	Glu	Tyr 325	Leu	Tyr	Ser	Gln	Asp 330	_	Ser	Phe	Tyr	Phe 335	Leu
Glu	Leu	Asn	Pro 340	Arg	Leu	Gln	Val	Glu 345	His	Pro	Cys	Thr	Glu 350	Met	Val
Ala	Asp	Val 355	Asn	Leu	Pro	Ala	Ala 360	Gln	Leu	Gln	Ile	Ala 365	Met	Gly	Ile
Pro	Leu 370	Tyr	Arg	Ile	Lys	Asp 375	Ile	Arg	Met	Met	Tyr 380	Gly	Val	Ser	Pro
Trp 385	_	Asp	Ser	Pro	Ile 390	Asp	Phe	Glu	Asp	Ser 395	Ala	His	Val	Pro	Cys 400
Pro	Arg	Gly	His	Val 405	Ile	Ala	Ala	Arg	Ile 410	Thr	Ser	Glu	Asn	Pro 415	Asp
Glu	Gly	Phe	Lys 420	Pro	Ser	Ser	Gly	Thr 425	Val	Gln	Glu	Leu	Asn 430	Phe	Arg
Ser	Asn	Lys 435	Asn	Val	Trp	Gly	Tyr 440	Phe	Ser	Val	Ala	Ala 445	Ala	Gly	Gly
Leu	His 450	Glu	Phe	Ala	Asp	Ser 455	Gln	Phe	Gly	His	Cys 460	Phe	Ser	Trp	Gly

Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp Leu Asp Arg Leu Ile Ala Glu Lys Val Gln <210> <211> 512 <212> PRT <213> Homo sapiens <220> <221> MISC_FEATURE <222> (2)..(512) N- and C-terminal deleted Human ACCasel BC domain (AAs 102-512) <223> <400> 59 Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asn Lys Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ser Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Leu Asp Ile Ala Lys Arg Ile Pro Val Gln Ala Val Trp Ala Gly Trp Gly His Ala

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Leu Lys Asn Gly Ile Ala

	130				:	135					140				
Ala 145	Ser	Ser	Ile	Val	Ala (150	Gln	Thr /	Ala	Gly	Ile 155	Pro	Thr	Leu	Pro	Trp 160
Ser	Gly	Ser	Gly	Leu 165	Arg '	Val	Asp	Trp	Gln 170	Glu	Asn	Asp	Phe	Ser 175	Lys
Arg	Ile	Leu	Asn 180	Val	Pro	Gln	Glu	Leu 185	Tyr	Glu	Lys	Gly	Tyr 190	Val	Lys
Asp	Val	Asp 195	Asp	Gly	Leu	Lys	Ala 200	Ala	Glu	Glu	Val	Gly 205	Tyr	Pro	Val
Met	Ile 210	Lys	Ala	Ser	Glu	Gly 215	Gly	Gly	Gly	Lys	Gly 220	Ile	Arg	Lys	Val
Asn 225		Ala	Asp	Asp	Phe 230	Pro	Asn	Leu	Phe	Arg 235	Gln	Val	Gln	Ala	Glu 240
Val	Pro	Gly	Ser	Pro 245		Phe	Val	Met	Arg 250	Leu	Ala	Lys	Gln	Ser 255	Arg
His	. Leu	Glu	Val 260	Gln	Ile	Leu	Ala	Asp 265	Gln	Tyr	Gly	Asn	Ala 270	Ile	Ser
Leu	ı Phe	e Gly 275		g Asp	Cys	Ser	Val 280	Gln	Arg	Arg	His	Gln 285	Lys	Ile	Ile
Glı	ı Glu 290		a Pro	o Ala	Thr	Ile 295		Thr	Pro) Ala	Val 300	Phe	e Glu	His	Met
Gl:		n Cya	s Ala	a Val	Lys 310		ı Ala	. Lys	Met	: Val	Gly	туг	val	Ser	Ala 320
Gl	y Th:	r Va	l Gl	u Tyi 325		туг	: Ser	Glr	a Asp 330	o Gly	y Ser	r Phe	∋ Туі	2 Phe 335	e Leu
Gl	u Le	u As	n Pr 34		g Lei	ı Glr	n Val	. Glu 345	ı His	s Pro	o Cys	s Thi	r Gli 350	ı Met	: Val
Al	a As	p Va 35		n Le	u Pro	o Ala	a Ala 360	a Glr	ı Le	u Gl	n Ile	e Ala 36	a Me ^s	t Gly	y Ile

Phe Met Gly Pro Pro Ser Gln Ala Met Trp Ala Leu Gly Asp Lys Ile

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Pro Leu Tyr Arg Ile Lys Asp Ile Arg Met Met Tyr Gly Val Ser Pro
    370
                        375
                                            380
Trp Gly Asp Ser Pro Ile Asp Phe Glu Asp Ser Ala His Val Pro Cys
385
                    390
                                        395
                                                             400
Pro Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp
                405
                                                         415
                                    410
Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg
            420
                                425
                                                     430
Ser Asn Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Gly Gly
        435
                            440
                                                445
Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly
    450
                        455
                                            460
Glu Asn Arg Glu Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu
465
                    470
                                        475
                                                             480
Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys
                485
                                    490
                                                         495
Leu Leu Glu Thr Glu Ser Phe Gln Met Asn Arg Ile Asp Thr Gly Trp
            500
                                505
                                                     510
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       60
<211>
       764
<212>
      PRT
<213> Homo sapiens
<220>
<221> MISC FEATURE
<222> (1)..(764)
      C-terminal deleted Human ACCase2 BC domain (AAs 1-764)
<223>
<400> 60
Met Val Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr
                                    10
                                                         15
Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile
            20
                                25
                                                    30
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Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe

Pro Al 50		Asp	Asn	Ser	Gly 55	Glu	Thr	Pro	Gln	Arg 60	Asn	Gly	Glu	Gly
His Th 65	r Leu	Pro	Lys	Thr 70	Pro	Ser	Gln	Ala	Glu 75	Pro	Ala	Ser	His	Lys 80
Gly Pr	o Lys	Asp	Ala 85	Gly	Arg	Arg	Arg	Asn 90	Ser	Leu	Pro	Pro	Ser 95	His
Gln Ly	s Pro	Pro 100	Arg	Asn	Pro	Leu	Ser 105	Ser	Ser	Asp	Ala	Ala 110	Pro	Ser
Pro Gl	u Leu 115	Gln	Ala	Asn	Gly	Thr 120	Gly	Thr	Gln	Gly	Leu 125	Glu	Ala	Thr
Asp Th		Gly	Leu	Śer	Ser 135	Ser	Ala	Arg	Pro	Gln 140	Gly	Gln	Gln	Ala
Gly Se 145	r Pro	Ser	Lys	Glu 150	Asp	Lys	Lys	Gln	Ala 155	Asn	Ile	Lys	Arg	Gln 160
Leu Me	t Thr	Asn	Phe 165	Ile	Leu	Gly	Ser	Phe 170	Asp	Asp	Tyr	Ser	Ser 175	Asp
Glu As	p Ser	Val 180	Ala	Gly	Ser	Ser	Arg 185	Glu	Ser	Thr	Arg	Lys 190	Gly	Ser
Arg Al	a Ser 195		Gly	Ala	Leu	Ser 200	Leu	Glu	Ala	Tyr	Leu 205	Thr	Thr	Gly
Glu Al 21		Thr	Arg	Val	Pro 215	Thr	Met	Arg	Pro	Ser 220	Met	Ser	Gly	Leu
His Le 225	u Val	Lys	Arg	Gly 230	Arg	Glu	His	Lys	Lys 235	Leu	Asp	Leu	His	Arg 240
Asp Ph	e Thr	Val	Ala 245	Ser	Pro	Ala	Glu	Phe 250	Val	Thr	Arg	Phe	Gly 255	Gly
Asp Ar	g Val	Ile 260	Glu	Lys	Val	Leu	Ile 265	Ala	Asn	Asn	Gly	Ile 270	Ala	Ala
Val Ly	s Cys 275	Met	Arg	Ser	Ile	Arg 280	Arg	Trp	Ala	Tyr	Glu 285	Met	Phe	Arg
Asn Gl	u Arg	Ala	Ile	Arg	Phe	Val	Val	Met	Val	Thr	Pro	Glu	Asp	Leu

Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val

Pro Gly Gly Pro Asn Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val

Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly

His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly

Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp

Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile

Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val

Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln

His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn

Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln

Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe

Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val <210> 61

<211> 754 <212> PRT

- <213> Homo sapiens
- <220>
- <221> MISC_FEATURE
- <222> (1)..(754)
- <223> C-terminal deleted Human ACCase2 BC domain (AAs 1-754)
- <400> 61
- Met Val Leu Leu Cys Leu Ser Cys Leu Ile Phe Ser Cys Leu Thr 1 10 15
- Phe Ser Trp Leu Lys Ile Trp Gly Lys Met Thr Asp Ser Lys Pro Ile 20 25 30
- Thr Lys Ser Lys Ser Glu Ala Asn Leu Ile Pro Ser Gln Glu Pro Phe 35 40 45
- Pro Ala Ser Asp Asn Ser Gly Glu Thr Pro Gln Arg Asn Gly Glu Gly 50 55 60
- His Thr Leu Pro Lys Thr Pro Ser Gln Ala Glu Pro Ala Ser His Lys 70 75 80
- Gly Pro Lys Asp Ala Gly Arg Arg Arg Asn Ser Leu Pro Pro Ser His
 85 90 95
- Gln Lys Pro Pro Arg Asn Pro Leu Ser Ser Ser Asp Ala Ala Pro Ser 100 105 110
- Pro Glu Leu Gln Ala Asn Gly Thr Gly Thr Gln Gly Leu Glu Ala Thr 115 120 125
- Asp Thr Asn Gly Leu Ser Ser Ser Ala Arg Pro Gln Gly Gln Gln Ala 130 135 140
- Gly Ser Pro Ser Lys Glu Asp Lys Lys Gln Ala Asn Ile Lys Arg Gln 145 150 150
- Leu Met Thr Asn Phe Ile Leu Gly Ser Phe Asp Asp Tyr Ser Ser Asp 165
- Glu Asp Ser Val Ala Gly Ser Ser Arg Glu Ser Thr Arg Lys Gly Ser 180 185 190
- Arg Ala Ser Leu Gly Ala Leu Ser Leu Glu Ala Tyr Leu Thr Thr Gly 195 200 205

His Leu Val Lys Arg Gly Arg Glu His Lys Lys Leu Asp Leu His Arg Asp Phe Thr Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu

Glu Ala Glu Thr Arg Val Pro Thr Met Arg Pro Ser Met Ser Gly Leu

Cys Val Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly
435 440 445

Pro Arg Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu

Gln Gln Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly

Phe Pro Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe 530 · Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe 690 695 700

Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala 705 710 715 720

Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr
725 730 735

Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp
740 745 750

Thr Gly

<210> 62

<211> 522

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (2)..(522)

<223> N- and C-terminal Human ACCase2 BC domain (AAs 224-764)

<400> 62

Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg
1 10 15

Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys 20 25 30

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 70 75 80

Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile 85 90 95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala

115 120 125

Phe	Leu	Gly	Pro	Pro	Ser	Glu	Ala	Met	Trp	Ala	Leu	Gly	Asp	Lys	Ile
	130	_				135					140				

- Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg 145 150 155 160
- Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln 165 170 175
- Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val 180 185 190
- Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro 195 200 205
- Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys 210 220
- Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser 225 230 235 240
- Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala 245 250 255
- Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val 260 265 270
- Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile 275 280 285
- Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe 290 295 300
- Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser 305 310 315 320
- Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe 325 330 335
- Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met 340 345 350
- Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly 355 360 365

Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly Trp Leu Asp Tyr Leu Ile Ala Glu Lys Val <210> 63 <211> 512 <212> PRT <213> Homo sapiens <220> <221> MIC FEATURE <222> (2)..(512) N- and C-terminal deleted Human ACCase2 BC domain (AAs 224-754) <223> <400> 63 Met Val Ala Ser Pro Ala Glu Phe Val Thr Arg Phe Gly Gly Asp Arg Val Ile Glu Lys Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys

Cys Met Arg Ser Ile Arg Arg Trp Ala Tyr Glu Met Phe Arg Asn Glu 35 40 45

Arg Ala Ile Arg Phe Val Val Met Val Thr Pro Glu Asp Leu Lys Ala 50 55 60

Asn Ala Glu Tyr Ile Lys Met Ala Asp His Tyr Val Pro Val Pro Gly 70 75 80

Gly Pro Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Ile 85 90 95

Ala Lys Arg Ile Pro Leu Gln Ala Val Trp Ala Gly Trp Gly His Ala 100 105 110

Ser Glu Asn Pro Lys Leu Pro Glu Leu Leu Cys Lys Asn Gly Val Ala 115 120 125

Phe Leu Gly Pro Pro Ser Glu Ala Met Trp Ala Leu Gly Asp Lys Ile 130 135 140

Ala Ser Thr Val Val Ala Gln Thr Leu Gln Val Pro Thr Leu Pro Arg 145 150 150

Ser Gly Ser Gly Leu Thr Val Glu Trp Thr Glu Asp Asp Leu Gln Gln 175

Gly Lys Arg Ile Ser Val Pro Glu Asp Val Tyr Asp Lys Gly Cys Val 180 185 190

Lys Asp Val Asp Glu Gly Leu Glu Ala Ala Glu Arg Ile Gly Phe Pro 195 200 205

Leu Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Lys 210 220

Ala Glu Ser Ala Glu Asp Phe Pro Ile Leu Phe Arg Gln Val Gln Ser 225 230 230 235 240

Glu Ile Pro Gly Ser Pro Ile Phe Leu Met Lys Leu Ala Gln His Ala 245 250 255

Arg His Leu Glu Val Gln Ile Leu Ala Asp Gln Tyr Gly Asn Ala Val 260 265 270

Val Glu Glu Ala Pro Ala Thr Ile Ala Pro Leu Ala Ile Phe Glu Phe Met Glu Gln Cys Ala Ile Arg Leu Ala Lys Thr Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser Gln Asp Gly Ser Phe His Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Cys Thr Glu Met Ile Ala Asp Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Val Pro Leu His Arg Leu Lys Asp Ile Arg Leu Leu Tyr Gly Glu Ser Pro Trp Gly Val Thr Pro Ile Ser Phe Glu Thr Pro Ser Asn Pro Pro Leu Ala Arg Gly His Val Ile Ala Ala Arg Ile Thr Ser Glu Asn Pro Asp Glu Gly Phe Lys Pro Ser Ser Gly Thr Val Gln Glu Leu Asn Phe Arg Ser Ser Lys Asn Val Trp Gly Tyr Phe Ser Val Ala Ala Thr Gly Gly Leu His Glu Phe Ala Asp Ser Gln Phe Gly His Cys Phe Ser Trp Gly Glu Asn Arg Lys Glu Ala Ile Ser Asn Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile

Ser Leu Phe Gly Arg Asp Cys Ser Ile Gln Arg Arg His Gln Lys Ile

Asn Leu Leu Glu Thr Glu Ser Phe Gln Asn Asn Asp Ile Asp Thr Gly

- <210> 64 <211> 521 <212> PRT <213> Magnaporthe grisea
- <220>
- <221> MISC_FEATURE
- <222> (1)..(521)
- <223> N-terminal deleted Magnaporthe ACCase BC domain (AAs 72-592)
- <400> 64
- Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 1 5 10 15
- Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala 20 25 30
- Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala 35 40 45
- Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 55 60
- Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80
- Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 95
- Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile 100 105 110
- Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile 115 120 125
- Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp 130 135 140
- Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val 145 150 155 160
- Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
 165 170 175
- Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys 180 185 190

Ala	Ser	Glu 195	Gly	Gly	Gly	Gly	Lys 200	Gly	Ile	Arg	Lys	Ala 205	Val	Ser	Glu
Glu	Gly 210	Phe	Glu	Glu	Leu	Tyr 215	Lys	Ala	Ala	Ala	Ser 220	Glu	Ile	Pro	Gly
Ser 225	Pro	Ile	Phe	Ile	Met 230	Lys	Leu	Ala	Gly	Asn 235	Ala	Arg	His	Leu	Glu 240
Val	Gln	Leu	Leu	Ala 245	Asp	Gln	Tyr	Gly	Asn 250	Asn	Ile	Ser	Leu	Phe 255	Gly
Arg	Asp	Cys	Ser 260	Val	Gln	Arg	Arg	His 265	Gln	Lys	Ile	Ile	Glu 270	Glu	Ala
Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	Tyr	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315		Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325		Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro 340	Ala	Ser	Gln	Leu	Gln 345		Ala	Met	Gly	Ile 350	Pro	Leu
His	Arg	Ile 355	Ser	Asp	Ile	Arg	Leu 360		Tyr	Gly	Val	Asp 365	Pro	Lys	Leu
Ser			Ile					Lys					Glu	Lys	Thr
Gln 385		Arg	Pro	Ser	Pro 390	Lys	Gly	His	Leu	Thr 395	Ala	Cys	Arg	Ile	Thr 400
Ser	Glu	Asp	Pro	Gly 405		Gly	Phe	Lys	Pro 410		Asn	Gly	Val	Met 415	His
Glu	Leu	Asn	Phe 420	Arg	Ser	Ser	Ser	Asn 425		Trp	Gly	Tyr	Phe 430	Ser	Val
(2) vz	Thr	Gln	Glv	Glv	Tle	His	Ser	Phe	Ser	Asn	Ser	Gln	Phe	Glv	His

435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr 485 490 495

Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr Ala 500 505 510

Glu Arg Pro Asp Lys Met Leu Ala Val 515 520

<210> 65

<211> 511

<212> PRT

<213> Magnaporthe grisea

<220>

<221> MISC_FEATURE

<222> (1)..(511)

<223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs 72-582)

<400> 65

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala 20 25 30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala 35 40 45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 55 60

Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 95

Asn	Pro	Lys	Leu 100	Pro	Glu	Ser	Leu	Ala 105	Ala	Ser	Pro	Lys	Lys 110	Ile	Ile
Phe	Ile	Gly 115	Pro	Pro	Gly	Ser	Ala 120	Met	Arg	Ser	Leu	Gly 125	Asp	Lys	Ile
Ser	Ser 130	Thr	Ile	Val	Ala	Gln 135	His	Ala	Gln	Val	Pro 140	Cys	Ile	Pro	Trp
Ser 145	Gly	Thr	Gly	Val	Asp 150	Ala	Val	Gln	Ile	Asp 155	Lys	Lys	Gly	Ile	Val 160
Thr	Val	Asp	Asp	Asp 165	Thr	Tyr	Ala	Lys	Gly 170	Cys	Val	Thr	Ser	Trp 175	Gln
Glu	Gly	Leu	Glu 180	Lys	Ala	Arg	Gln	Ile 185	Gly	Phe	Pro	Val	Met 190	Ile	Lys
Ala	Ser	Glu 195	Gly	Gly	Gly	Gly	Lys 200	Gly	Ile	Arg	Lys	Ala 205	Val	Ser	Glu
Glu	Gly 210	Phe	Glu	Glu	Leu	Tyr 215	Lys	Ala	Ala	Ala	Ser 220	Glu	Ile	Pro	Gly
Ser 225	Pro	Ile	Phe	Ile	Met 230	Lys	Leu	Ala	Gly	Asn 235	Ala	Arg	His	Leu	Glu 240
Val	Gln	Leu	Leu	Ala 245	Asp	Gln	Tyr	Gly	Asn 250	Asn	Ile	Ser	Leu	Phe 255	Gly
Arg	Asp	Cys	Ser 260	Val	Gln	Arg	Arg	His 265	Gln	Lys	Ile	Ile	Glu 270	Glu	Ala
Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	Tyr	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315	Tyr	Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325	Val	Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro	Ala	Ser	Gln	Leu	Gln	Ile	Ala	Met	Gly	Ile	Pro	Leu

340 345 350

His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu 355 360 365

Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr 370 380

Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr 385 390 395 400

Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His
405 410 415

Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val
420 425 430

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His
435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr 485 490 495

Ile Thr Thr Gly Trp Leu Asp Glu Leu Ile Ser Lys Lys Leu Thr
500 505 510

<210> 66

<211> 501

<212> PRT

<213> Magnaporthe grisea

<220>

<221> misc feature

<223> N- and C-terminal deleted Magnaporthe ACCase BC domain (AAs
72-572)

<400> 66

Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 1 5 10 15

Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala

25

20

30

Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala 35 40 45

Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 60

Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80

Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 95

Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile 100 105 110

Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile 115 120 125

Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp 130 135 140

Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val 145 150 150

Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
165 170 175

Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys 180 185 190

Ala Ser Glu Gly Gly Gly Lys Gly Ile Arg Lys Ala Val Ser Glu 195 200 205

Glu Gly Phe Glu Glu Leu Tyr Lys Ala Ala Ala Ser Glu Ile Pro Gly 210 215 220

Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Asn Ala Arg His Leu Glu 225 230 235 240

Val Gln Leu Leu Ala Asp Gln Tyr Gly Asn Asn Ile Ser Leu Phe Gly 255

Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala 260 265 270

Pro Val Thr Ile Ala Lys Pro Asp Thr Phe Lys Ala Met Glu Glu Ala Ala Val Arg Leu Gly Arg Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Ala Asp Asp Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Gly Val Ser Gly Val Asn Leu Pro Ala Ser Gln Leu Gln Ile Ala Met Gly Ile Pro Leu His Arg Ile Ser Asp Ile Arg Leu Leu Tyr Gly Val Asp Pro Lys Leu Ser Thr Glu Ile Asp Phe Asp Phe Lys Asn Pro Asp Ser Glu Lys Thr Gln Arg Arg Pro Ser Pro Lys Gly His Leu Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Gly Glu Gly Phe Lys Pro Ser Asn Gly Val Met His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala Phe Glu Glu Asn Thr

Ile Thr Thr Gly Trp

- <210> 67
- <211> 491
- <212> PRT
- <213> Magnaporthe grisea
- <220>
- <221> MISC FEATURE
- <222> (1)..(491)
- <223> N- and C-terminal deleted ACCase BC domain (AAs 72-562)
- <400> 67
- Thr Asn Val Leu Ile Ala Asn Asn Gly Ile Ala Ala Val Lys Glu Ile 1 5 10 15
- Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp Glu Arg Ala 20 25 30
- Ile Gln Phe Thr Val Met Ala Thr Pro Glu Asp Leu Gln Ala Asn Ala 35 40 45
- Asp Tyr Ile Arg Met Ala Asp His Tyr Val Glu Val Pro Gly Gly Thr 50 55 60
- Asn Asn Asn Tyr Ala Asn Val Glu Leu Ile Val Asp Val Ala Glu 65 70 75 80
- Arg Met Asn Val His Ala Val Trp Ala Gly Trp Gly His Ala Ser Glu 85 90 95
- Asn Pro Lys Leu Pro Glu Ser Leu Ala Ala Ser Pro Lys Lys Ile Ile 100 105 110
- Phe Ile Gly Pro Pro Gly Ser Ala Met Arg Ser Leu Gly Asp Lys Ile 115 120 125
- Ser Ser Thr Ile Val Ala Gln His Ala Gln Val Pro Cys Ile Pro Trp 130 135 140
- Ser Gly Thr Gly Val Asp Ala Val Gln Ile Asp Lys Lys Gly Ile Val 145 150 150
- Thr Val Asp Asp Asp Thr Tyr Ala Lys Gly Cys Val Thr Ser Trp Gln
 165 170 175
- Glu Gly Leu Glu Lys Ala Arg Gln Ile Gly Phe Pro Val Met Ile Lys 180 185 190

Ala	Ser	Glu 195	Gly	Gly	Gly	Gly	Lys 200	Gly	Ile	Arg	Lys	Ala 205	Val	Ser	Glu
Glu	Gly 210	Phe	Glu	Glu	Leu	Tyr 215	Lys	Ala	Ala	Ala	Ser 220	Glu	Ile	Pro	Gly
Ser 225	Pro	Ile	Phe	Ile	Met 230	Lys	Leu	Ala	Gly	Asn 235	Ala	Arg	His	Leu	Glu 240
Val	Gln	Leu	Leu	Ala 245	Asp	Gln	Tyr	Gly	Asn 250	Asn	Ile	Ser	Leu	Phe 255	Gly
Arg	Asp	Cys	Ser 260	Val	Gln	Arg	Arg	His 265	Gln	Lys	Ile	Ile	Glu 270	Glu	Ala
Pro	Val	Thr 275	Ile	Ala	Lys	Pro	Asp 280	Thr	Phe	Lys	Ala	Met 285	Glu	Glu	Ala
Ala	Val 290	Arg	Leu	Gly	Arg	Leu 295	Val	Gly	Tyr	Val	Ser 300	Ala	Gly	Thr	Val
Glu 305	_	Leu	Tyr	Ser	His 310	Ala	Asp	Asp	Lys	Phe 315	Tyr	Phe	Leu	Glu	Leu 320
Asn	Pro	Arg	Leu	Gln 325	Val	Glu	His	Pro	Thr 330	Thr	Glu	Gly	Val	Ser 335	Gly
Val	Asn	Leu	Pro 340	Ala	Ser	Gln	Leu	Gln 345	Ile	Ala	Met	Gly	Ile 350	Pro	Leu
His	Arg	Ile 355	Ser	Asp	Ile	Arg	Leu 360	Leu	Tyr	Gly	Val	Asp 365	Pro	Lys	Leu
Ser	Thr 370	Glu	Ile	Asp	Phe	Asp 375	Phe	Lys	Asn	Pro	Asp 380	Ser	Glu	Lys	Thr
Gln 385	Arg	Arg	Pro	Ser	Pro 390	Lys	Gly	His	Leu	Thr 395	Ala	Cys	Arg	Ile	Thr 400
Ser	Glu	Asp	Pro	Gly 405	Glu	Gly	Phe	Lys	Pro 410	Ser	Asn	Gly	Val	Met 415	His
Glu	Leu	Asn	Phe 420	Arg	Ser	Ser	Ser	Asn 425	Val	Trp	Gly	Tyr	Phe 430	Ser	Val

Gly Thr Gln Gly Gly Ile His Ser Phe Ser Asp Ser Gln Phe Gly His
435 440 445

Ile Phe Ala Tyr Gly Glu Asn Arg Ser Ala Ser Arg Lys His Met Val 450 455 460

Ile Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val
465 470 475 480

Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Ala 485 490

<210> 68

<211> 525

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(525)

<223> N-terminal deleted Yeast ACCase BC domain (AAs--57-581)

<400> 68

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val 1 5 10 15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 20 25 30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu 35 40 45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro 50 60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 100 105 110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly 115 120 125

Asp	Lys 130	Ile	Ser	Ser	Thr	Ile 135	Val	Ala	Gln	Ser	Ala 140	Lys	Val	Pro	Cys
Ile 145	Pro	Trp	Ser	Gly	Thr 150	Gly	Val	Asp	Thr	Val 155	His	Val	Asp	Glu	Lys 160
Thr	Gly	Leu	Val	Ser 165	Val	Asp	Asp	Asp	Ile 170	Tyr	Gln	Lys	Gly	Cys 175	Cys
Thr	Ser	Pro	Glu 180	Asp	Gly	Leu	Gln	Lys 185	Ala	Lys	Arg	Ile	Gly 190	Phe	Pro
Val	Met	Ile 195	Lys	Ala	Ser	Glu	Gly 200	Gly	Gly	Gly	Lys	Gly 205	Ile	Arg	Gln
Val	Glu 210	Arg	Glu	Glu	Asp	Phe 215	Ile	Ala	Leu	Tyr	His 220	Gln	Ala	Ala	Asn
Glu 225	Ile	Pro	Gly	Ser	Pro 230	Ile	Phe	Ile	Met	Lys 235	Leu	Ala	Gly	Arg	Ala 240
Arg	His	Leu	Glu	Val 245	Gln	Leu	Leu	Ala	Asp 250	Gln	Tyr	Gly	Thr	Asn 255	Ile
Ser	Leu	Phe	Gly 260	Arg	Asp	Cys	Ser	Val 265	Gln	Arg	Arg	His	Gln 270	Lys	Ile
Ile	Glu	Glu 275	Ala	Pro	Val	Thr	Ile 280	Ala	Lys	Ala	Glu	Thr 285	Phe	His	Glu
	Glu 290	_				295			_		300	_	_		
305	Gly				310					315					320
Phe	Leu	Glu	Leu	Asn 325	Pro	Arg	Leu	Gln	Val 330	Glu	His	Pro	Thr	Thr 335	Glu
Met	Val	Ser	Gly 340	Val	Asn	Leu	Pro	Ala 345	Ala	Gln	Leu	Gln	Ile 350	Ala	Met
Gly	Ile	Pro 355	Met	His	Arg	Ile	Ser 360	Asp	Ile	Arg	Thr	Leu 365	Tyr	Gly	Met
Asn	Pro	His	Ser	Ala	Ser	Glu	Ile	Asp	Phe	Glu	Phe	Lys	Thr	Gln	Asp

370 375 380

Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala 385 390 395 400

Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly 405 410 415

Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly
420 425 430

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser 435 440 445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg 450 455 460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 470 475 480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe 485 490 495

Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His
500 505 510

Lys Met Thr Ala Glu Lys Pro Asp Pro Thr Leu Ala Val 515 520 525

<210> 69

<211> 515

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(515)

<223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-571)

<400> 69

Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val 1 5 10 15

Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 20 25 30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu

35 40 45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro 50 60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 100 105 110

Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly 115 120 125

Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys 130 135 140

Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
145 150 155 160

Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys 165 170 175

Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro 180 185 190

Val Met Ile Lys Ala Ser Glu Gly Gly Gly Gly Lys Gly Ile Arg Gln 195 200 205

Val Glu Arg Glu Glu Asp Phe Ile Ala Leu Tyr His Gln Ala Ala Asn 210 215 220

Glu Ile Pro Gly Ser Pro Ile Phe Ile Met Lys Leu Ala Gly Arg Ala 225 230 235 240

Arg His Leu Glu Val Gln Leu Leu Ala Asp Gln Tyr Gly Thr Asn Ile 245 250 255

Ser Leu Phe Gly Arg Asp Cys Ser Val Gln Arg Arg His Gln Lys Ile 260 265 270

Ile Glu Glu Ala Pro Val Thr Ile Ala Lys Ala Glu Thr Phe His Glu 275 280 285

Met Glu Lys Ala Ala Val Arg Leu Gly Lys Leu Val Gly Tyr Val Ser Ala Gly Thr Val Glu Tyr Leu Tyr Ser His Asp Asp Gly Lys Phe Tyr Phe Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Thr Thr Glu Met Val Ser Gly Val Asn Leu Pro Ala Ala Gln Leu Gln Ile Ala Met Gly Ile Pro Met His Arg Ile Ser Asp Ile Arg Thr Leu Tyr Gly Met Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe Glu Asp Asn Thr Ile Thr Thr Gly Trp Leu Asp Asp Leu Ile Thr His

Lys Met Thr

- <210> 70
- <211> 505
- <212> PRT
- <213> Saccharomyces cerevisiae
- <220>
- <221> MISC FEATURE
- <222> (1)..(505)
- <223> N- and C-terminal deleted Yeast ACCase BC domain (AAs 57-561)
- <400> 70
- Thr Val Ile Ser Lys Ile Leu Ile Ala Asn Asn Gly Ile Ala Ala Val 1 5 10 15
- Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 20 25 30
- Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu 35 40 45
- Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro
 50 55 60
- Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 75 80
- Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
 85 90 95
- Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 100 105 110
- Lys Val Ile Phe Ile Gly Pro Pro Gly Asn Ala Met Arg Ser Leu Gly 115 120 125
- Asp Lys Ile Ser Ser Thr Ile Val Ala Gln Ser Ala Lys Val Pro Cys 130 135 140
- Ile Pro Trp Ser Gly Thr Gly Val Asp Thr Val His Val Asp Glu Lys
 145 150 155 160
- Thr Gly Leu Val Ser Val Asp Asp Asp Ile Tyr Gln Lys Gly Cys Cys 165 170 175
- Thr Ser Pro Glu Asp Gly Leu Gln Lys Ala Lys Arg Ile Gly Phe Pro 180 185 190

Val	Met	Ile 195	Lys	Ala	Ser	Glu	Gly 200	Gly	Gly	Gly	Lys	Gly 205	Ile	Arg	Gln
Val	Glu 210	Arg	Glu	Glu	Asp	Phe 215	Ile	Ala	Leu	Tyr	His 220	Gln	Ala	Ala	Asn
Glu 225	Ile	Pro	Gly	Ser	Pro 230	Ile	Phe	Ile	Met	Lys 235	Leu	Ala	Gly	Arg	Ala 240
Arg	His	Leu	Glu	Val 245	Gln	Leu	Leu	Ala	Asp 250	Gln	Tyr	Gly	Thr	Asn 255	Ile
Ser	Leu	Phe	Gly 260	Arg	Asp	Cys	Ser	Val 265	Gln	Arg	Arg	His	Gln 270	Lys	Ile
Ile	Glu	Glu 275	Ala	Pro	Val	Thr	Ile 280	Ala	Lys	Ala	Glu	Thr 285	Phe	His	Glu
Met	Glu 290		Ala	Ala	Val	Arg 295		Gly	Lys	Leu	Val 300	Gly	Tyr	Val	Ser
Ala 305	_	Thr	Val	Glu	Tyr 310	Leu	Tyr	Ser	His	Asp 315		Gly	Lys	Phe	Tyr 320
Phe	Leu	Glu	Leu	Asn 325	Pro	Arg	Leu	Gln	Val 330		His	Pro	Thr	Thr 335	Glu
Met	Val	Ser	Gly 340		Asn	Leu	Pro	Ala 345		Gln	Leu	Gln	Ile 350		Met
Gly	Ile	Pro 355		His	Arg	Ile	Ser 360		Ile	Arg	Thr	Leu 365		Gly	Met
Asn	Pro 370		Ser	Ala	Ser	Glu 375		Asp	Phe	Glu	Phe 380		Thr	Gln	Asp
Ala 385		Lys	Lys	Gln	Arg 390		Pro	Ile	Pro	Lys 395		His	Cys	Thr	Ala 400
Cys	Arg	Ile	Thr	Ser 405	Glu	Asp	Pro	Asn	Asp 410		Phe	. Lys	Pro	Ser 415	
Gly	Thr	Leu	His 420		. Leu	Asn	Phe	Arg		Ser	Ser	Asn	Val 430		Gly

Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser 435 440 445

Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg 450 455 460

Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 465 470 480

Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp Phe 485 490 495

Glu Asp Asn Thr Ile Thr Thr Gly Trp
500 505

<210> 71

<211> 495

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<221> MISC FEATURE

<222> (1)..(495)

<223> N- and C-terminal deleted YEast ACCase BC domain (AAs 57-551)

<400> 71

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Lys Glu Ile Arg Ser Val Arg Lys Trp Ala Tyr Glu Thr Phe Gly Asp 20 25 30

Asp Arg Thr Val Gln Phe Val Ala Met Ala Thr Pro Glu Asp Leu Glu 35 40 45

Ala Asn Ala Glu Tyr Ile Arg Met Ala Asp Gln Tyr Ile Glu Val Pro 50 60

Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Asp Leu Ile Val Asp 65 70 75 80

Ile Ala Glu Arg Ala Asp Val Asp Ala Val Trp Ala Gly Trp Gly His
85 90 95

Ala Ser Glu Asn Pro Leu Leu Pro Glu Lys Leu Ser Gln Ser Lys Arg 100 105 110

Lys	Val	116		e Ile	e GIY	Pro	Pro 120		Asn	ı Ala	Met	125		Lev	ı Gly
Asp	Lys 130		: Ser	Ser	Thr	Ile 135		Ala	Gln	Ser	Ala 140		Val	. Pro	Cys
Ile 145		Trp	Ser	Gly	Thr 150		Val	Asp	Thr	Val 155		Val	Asp	Glu	160
Thr	Gly	Leu	. Val	Ser 165	Val	Asp	Asp	Asp	Ile 170		Gln	Lys	Gly	Cys 175	_
Thr	Ser	Pro	Glu 180		Gly	Leu	Gln	Lys 185		Lys	Arg	Ile	Gly 190		Pro
Val	Met	Ile 195		Äla	Ser	Glu	Gly 200		Gly	Gly	Lys	Gly 205		Arg	Gľn
Val	Glu 210		Glu	Glu	Asp	Phe 215		Ala	Leu	Tyr	His 220		Ala	Ala	Asn
Glu 225		Pro	Gly	Ser	Pro 230	Ile	Phe	Ile	Met	Lys 235		Ala	Gly	Arg	Ala 240
Arg	His	Leu	Glu	Val 245	Gln	Leu	Leu	Ala	Asp 250		Tyr	Gly	Thr	Asn 255	
Ser	Leu	Phe	Gly 260		Asp	Cys	Ser	Val 265	Gln	Arg	Arg	His	Gln 270	Lys	Ile
Ile	Glu	Glu 275	Ala	Pro	Val	Thr	Ile 280	Ala	Lys	Ala	Glu	Thr 285	Phe	His	Glu
Met	Glu 290				Val										Ser
Ala 305	Gly	Thr	Val	Glu	Tyr 310	Leu	Tyr	Ser	His	Asp 315	Asp	Gly	Lys	Phe	Tyr 320
Phe	Leu	Glu	Leu	Asn 325	Pro	Arg	Leu	Gln	Val 330	Glu	His	Pro	Thr	Thr 335	Glu
Met	Val	Ser	Gly 340	Val	Asn	Leu	Pro	Ala 345	Ala	Gln	Leu	Gln	Ile 350	Ala	Met
Gly	Ile	Pro	Met	His	Arg	Ile	Ser	Asp	Ile	Ara	Thr	Leu	Tvr	Glv	Met

355 360 365

Asn Pro His Ser Ala Ser Glu Ile Asp Phe Glu Phe Lys Thr Gln Asp 370 380

- Ala Thr Lys Lys Gln Arg Arg Pro Ile Pro Lys Gly His Cys Thr Ala 385 390 395 400
- Cys Arg Ile Thr Ser Glu Asp Pro Asn Asp Gly Phe Lys Pro Ser Gly 405 410 415
- Gly Thr Leu His Glu Leu Asn Phe Arg Ser Ser Ser Asn Val Trp Gly 420 425 430
- Tyr Phe Ser Val Gly Asn Asn Gly Asn Ile His Ser Phe Ser Asp Ser 435 440 445
- Gln Phe Gly His Ile Phe Ala Phe Gly Glu Asn Arg Gln Ala Ser Arg 450 455 460
- Lys His Met Val Val Ala Leu Lys Glu Leu Ser Ile Arg Gly Asp Phe 465 470 475 480
- Arg Thr Thr Val Glu Tyr Leu Ile Lys Leu Leu Glu Thr Glu Asp 485 490 495